

865

GGAGATGAAA	AAGAGATTGA	CACCTCATCT	TTAATCAGCG	TAGAGGGTAA	TGTTGAAGGT	240
TATGAACTT	TTAGCGACTC	GCTTTTTTTG	CTCTCTAAAG	AAAGGATTGA	AGAAGCCCTT	300
CATTATTACC	AGCCTAAAAA	AGTCTATAAT	TTAAGCTATG	GGGCGAAAAT	CAAGCACGCC	360
GTTAGCCTCA	ATCACTCTCA	AGTGAAATG	AAACAAATCA	ACAAACAAGA	CGCTATCGTT	420
CGCATTAATA	GCATGTTTAG	CCCTAGAAGT	AATCATGCTA	AGGATTTAAA	AAATTTACAA	480
AAAAATCTGA	TTCGTTTAA	AGAGGATTTT	TTACGCGCAT	TAAACACGCC	TTGTAAAACC	540
AAGCAAGAAG	CATTGGAATG	GGTGGATAGC	TTGAGTGGAT	TTTGCCAAAC	AGCCAGCGCT	600
AAAACCCCCA	CTATAGGCAT	TTTATTGAA	GGGAGTGTG	CCCATATCTT	ACAAAGCGTT	660
CTAATCGTTT	CATTGCATCT	TAAAGAAAAT	GAGCTGACGC	TTTTATCAAA	TTCTCTCAAA	720
ACGCCT						726

(2) INFORMATION FOR SEQ ID NO:1206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206

ATCCTTCTTG	TTGAATTAAA	GTTACACCCT	AAGATCGGTT	ATTTTTCTAA	AAGATTTAAT	60
TTTTTATCAA	AGATGAGGGT	TTTAGAGTGG	AAATATTGGT	TAAATACTGA	TAAGTGGGAT	120
ACGCCCCACA	ACAAACCGCC	TCAAACCTTT	AAAATACAAA	TTTTTAAGAT	ACAAATAGGT	180
ATAATCAATA	ACTTCAATCA	TTTAATCAAA	GGGAGTTCTA	TGAAAAACGC	TTTCAAAGCG	240
TTTGCCCTGT	TAATCGTATT	TTTCTCAAAC	GCTCTATTAG	CGCAGGATTT	AAAAATCGCT	300
GCTGCTGCTA	ATCTCACGCG	CGCTTTAAAA	GCCCTTGTTA	AAGAATTTCA	AAAAGAACAC	360
CCAAAAGACG	CTATTAACAT	TAGCTTTAAT	TCTTCAGGCA	AACCTCTACG	TCAAATCGCT	420
CAAAACGCCC	CTTTTGATTT	ATTCAATTTCA	GCGGATATTG	CTAGACCCAA	AAAACTTTAT	480
GATGAAAAAA	TAACCCCTTT	TAAAGAAGAA	GTCTATGCTA	AAGGCGTGTT	GGTTTTATGG	540
AGTGAAAATC	TAAAAATGGA	TTCTTTAGAA	ATTCTTAAAG	ACCCTAAAAT	TAAACGTATC	600
GCTATGGCTA	ATCCTAAACT	AGCCCTTAT	GGAAAAGCCA	GCATGGAAGT	CTTGATCGT	660
TTAAACTCA	CTCCTAGTCT	TAAATCTAAA	ATCATTATG	GCGCTTCTAT	TTCTCAAGCC	720
CATCAATTCA	TCGCCACCAA	AAACGCTCAA	ATAGGCTTTG	GAGCGTTATC	TTTGATCGAT	780
AAAAAAGACA	AAACCTCTC	TTATTTCATC	ATTGATAAAA	CCCTTTATAA	CCCTATTGAA	840
CAAGCCTTAA	TCATCACTAA	AAATGGGGCT	AATAACCCTT	TAGCCAAAGT	TTTTAAAGAT	900
TTTTTATTCA	GCCCTAAAGC	TAGAGCTATC	TTTAAAGAAT	ACGGCTATAT	TGTGGAT	957

(2) INFORMATION FOR SEQ ID NO:1207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

866

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207

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AAAAGGCGAA CAATGGATCA TGAGTTTTTG ATTACCATGC GTTTGAGCTT TTCTTTAGCT      60
TTGATTACCA CCCTTATTTT ACTCCCTATA GGGATTTTTT TAGGCTATTT TTTAAGCCTT      120
AAACGCAATC TTTTAACGAG CTTAACAGAA ACGCTTGTTG ATATGCCTTT AGTTTTACCC      180
CCAAGCGTGC TAGGGTTTTA TCTTCTTTTA ATCTTTTCGC CTTCTTCTTT TTGGGAGCG      240
TTTTTACAAG ATGTGTTAAA TGTGAACTC GTTTTTAGTT TCCAAGGGCT TATCTTAGGG      300
AGCGTGATTT TTTCTTGCC CTTTATGGTA AGCCCTATTA AAAGCGCGTT AATTTCTTG      360
CCCCTTCTT TAAAAGAAGC CAGTTATAGC TTGGGTAAAG GGAATACTA CACCTTTTT      420
TTTGTCCTAC TCCCTAACAT CAAACCCAGT GTGTGATGG CTATCATTAC AACTTTTATG      480
CACACTATAG GTGAATTTGG CGTGGTGATG ATGCTTGGGG GTGATATATT AGGGGAAACA      540
AGAGTGGCTA GCATTACGAT CTTTAACGAA GCTGAAGCAC TCAATTATTC TAAAGCCCAT      600
CAATACGCCT TAACGCTCAC GCTTATTAGT TTTAGCCTCT TGTTTGTTAC CCTATTTTAA      660
AATAAAAAAC AAAGCTCGTT TTTA                                     684
  
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(2) INFORMATION FOR SEQ ID NO:1208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 561 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208

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AATTTTATTT TTGGAGAATT TATAATGAAG AGATCTTCTG TATTTAGTTT CTTGGTAGCT      60
TTTTTATTGG TAGTTGGCTG TAGTCATAAA ATGGATAATA AGACTGTGGC TGGCGATGTG      120
AGCACTAAAG CGGTTCAAGC TGCCTGCTGTT ACTACAGAAC CAGCTCCAGA GAAAGAAGAG      180
CCTAAACAAG AGCCAGCTCC AGTGGTTGAA GAAAAGCCGG CTATTGAAAG CGGGACTATC      240
ATCGCTTCTA TTTATTTTGA TTTTGACAAG TATGAGATCA AAGAATCCGA TCAAGAGACT      300
TTAGATGAGA TCGTGCAAAA AGCTAAAGAA AACCACATGC AAGTGCTTTT GGAAGGCAAT      360
ACCGATGAAT TTGGCTCTAG CGAATACAAC CAAGCGCTTG GCGTTAAAAG GACTTTGAGC      420
GTGAAAAACG CTTTAGTCAT TAAAGGGGTA GAAAAAGATA TGATCAAAAC CATCAGTTTT      480
GGCGAAAGCA AACCCAAATG CGTCCAAAAA ACTAGAGAAT GTTACAGAGA AAACAGAAGA      540
GTGGATGTCA AATTAGTGAA G                                     561
  
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(2) INFORMATION FOR SEQ ID NO:1209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 603 base pairs
 (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

867

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209

AAACGAATCA	AAAGAGGGTT	TTTTATGCAA	GAAGCGTTGT	TGCGTTTTCA	AGAGGGCTTT	60
AAGGAGTGGG	GTTATCTTAT	TTTATTTTGG	TATTCCTTGG	GGGGTGGGTA	TGTAGGGATT	120
GTCAATCGCTT	CCATTTTGAG	CGCTACCACG	CACGCTTTGG	ATATAAAAAT	AACCATTTCTT	180
GTCGCTTTTT	TAGGGAATTT	AATAGGGAGT	GGGGCTCTTG	TAATCTTTGC	CCGCTATCAA	240
AAAAGAGAGT	TTTTAAAGTA	TTTCCAAAAG	CATAGAAGAA	AGCTTGCTTT	GGCGAGTTTG	300
TGGGTGAAAC	GCTACGCCTT	GCTCATGATT	TTGTCAATA	AATATCTCTA	TGGGATTAAA	360
AGCGTTGTGC	CTTTGGCAAT	TGGTTTTAGC	AAATACCCCT	TAAAAAAGTT	TTTATGGCTT	420
AATGTTTTTT	CCAGTTTTTT	GTGGGCGTTA	ATCGTGGGGA	GCGTTTCCTT	TCAAGCGAGC	480
GATTGGGTGA	AAACGCTGTA	TGAAAGGCTT	TCTCATTACA	CTTCGTTTTT	TGTCATAAGT	540
TTTGTTCTTA	TAGCGCTTTT	AATATGGTTT	TTATTGAAAC	GATATTCGCG	CAAAATGGGT	600
TTT						603

(2) INFORMATION FOR SEQ ID NO:1210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210

GCTAGTTTTA	ATTACAATTT	TCAAATGTTA	AGGAAAAACA	TTTTAGCTTA	CTATGGGGCG	60
AATTTTCTCT	TAATCATCGC	TCAAAGCTTG	CCCCATGCCA	TTTTAACCCC	CTGTGTGCTT	120
TCTAAAGGGC	TTAGTTTGAG	TGAAATCTTG	CTCGTGCAAA	CCTTTTTTAG	TTTTTGCGTG	180
CTGGTGGCTG	AATACCCAAG	CGCGTTTTTA	GCGGATTTGA	TGAGCCGGAA	GAATTTATTC	240
CTGTTTCTTA	ATGTGTTTTT	AATCGCTAGT	TTTTCGTTTG	TGCTGTTTTT	TGATAGTTTT	300
ATCCTCATGC	TTTTAGCGTG	GGGTTGTAT	GGTTTGTTATA	GCGCATGCTC	TAGCGGCACG	360
ATTGAAGCTT	CACTCATCAC	AGACATTAAG	GAAAAACAAA	AAGATTTATC	CAAGTTTTTA	420
GCCAAAAACA	ATCAAATTAC	TTATTTGGGC	ATGATTATAG	GGAGTTCTTT	GGGATCGTTT	480
TTGTATCTCA	AAGTCCATGC	GATGCTGTAT	GTCGTGGGGA	TTTTTTTAAT	CATGCTCTGT	540
GCGCTAACAA	TCATCATTTA	TTTTAAAGAA	AAAGAAGGGG	ATTTTAAAAG	CCAAAAAAT	600
TTGAACTCC	TTAAAGAGCA	AGTCAAAGGC	AGTCTTAAAG	AGCTTAAAGA	TAACCCCAAG	660

SUBSTITUTE SHEET (RULE 26)

868

CTTAAATTT	TGTTAGTGGG	GCATTTGATT	ACGCCTGTCT	TTTTTATGAG	CCATTTCCAA	720
ATGTGGCAAG	CGTATTTTT	AAAACAAGGC	GTAAAGAGC	AATACCTTTT	TGTGTTCTAT	780
ATCGCTTTT	AAGTGATTT	CATCCTCATT	CATTTTTTAA	AAGCCAAAAA	TTACAGCCAA	840
AAAATCGCCC	TGAGTTCGCT	TTTGGTGTG	CTAGGCGTTA	GCCCCTTGTT	GCTTAGCAAT	900
ATCCCTTATT	GTTTCATAGG	GGTGATGCG	CTCATGGTGG	CGTTTTTTGC	TTACATGAGT	960
TATTGCTTGG	GGTATCAATT	CTCCAAATTC	GTTTCTAAAA	ACAACATTTC	ATCGCTCTCA	1020
TCGCTTTTAT	CAAGCTGTGT	GCGCGTGGTC	TCTGTGCTAA	TCTTGTGCGT	CAGTAGCCTA	1080
GAGTTCGCTT	ACTTCTCACC	CCTAATCATC	ATAACCATGC	ATTTTGCCCT	AACGCTTATC	1140
ATCCTCTTTT	TCTTTTTGTA	TAAGGCTAAG	CCGTTTGATG	AG		1182

(2) INFORMATION FOR SEQ ID NO:1211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211

CGCAGAAATC	TTACTAGACA	ACATGGAAGT	GTAAAAAGC	GTGAGAAGCG	TTTTAAAACG	60
CATGCGAGCC	TTTGCGATAG	CGTGAGGAGC	GGTAAAAGAT	TAGGCTATAC	CAATCAAGTG	120
ATCACCATA	TTGTCAATAT	CGGTATTGGG	GGGTCAGATT	TAGGCGCTTT	AATGGTTTGC	180
ACCGCCCTAA	AACGCTACGG	CCACCCAAGA	TTAGAAATGC	ATTTTGTGTC	TAATGTGGAT	240
GGCAGCAGA	TTTTAGACGT	T				261

(2) INFORMATION FOR SEQ ID NO:1212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212

CAGCATTATC	CTAATAACCT	AAAAGATATA	GAGATGAATA	CAGAAATTTT	AACCATCATG	60
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SUBSTITUTE SHEET (RULE 26)

869

TTAGTTGTCT	CCGTGCTTAT	GGGATTGGTA	GGCTTAATAG	CGTTTTTATG	GGGGGTAA	120
AGCGGTCAGT	TTGACGATGA	AAAACGCATG	CTTGAAAGCG	TGTTGTATGA	CAGCGCGAGC	180
GACTTGAACG	AAGCGATTTT	ACAAGAAAAA	CGCCAAAAGA	AT		222

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213

GAAATGCAGT	TTTTACATGC	GCATCTTTTA	AGCGTGGTGA	TCTTTTTCCC	CATGCTGAGC	60
GCTCTATTAG	CGTTCCTTAT	GAGCGATCAA	GCGAGCAGGG	CGTATGCGAT	CGTCATCGCC	120
TTGATTGAAT	TGTTATTGGT	CTTGTTGTTA	TGGCATGGGT	TTGATATTCA	AACCGCAGGC	180
ATGCAGTTTG	AAGAAATGAA	AGAATTAGCC	TATCAAATTG	GCGTGAATTA	CCATGTTGGC	240
GTTGATGGCA	TCCGCTCTTT	TTGTTGCTC	TTAAACGCTA	TCGTGGTGTT	ATTGTCCGTG	300
ATTTATGTCA	AAGAGCGTCG	TAAAGACTTT	GTGATTTGTC	TTTTATTGTT	AGAAGGGATC	360
TTAATGGGCG	TGTTTTCTTC	TCTTAATGTG	ATCTTTTTCT	ACGCTTTTTG	GGAAATCTCG	420
CTCTTGCCGG	TTTTATACCT	CATCGGTCGT	TTTGGCCGTA	ATAACAAAAT	CTATTCTGGC	480
ATGAAGTTTT	TCCTCTACAC	CTTTTTAGCG	TCGTTGTGCA	TGCTTTTAGG	CATTTTATAC	540
ATCGGGTATG	ACTACGCCAA	TAATTACGGC	ATGATGAGTT	TTGATATTTT	AGACTGGTAT	600
CAGTTGAATT	TTTCTAGCGG	GATTAAACC	TGGCTCTTTG	TAGCTTCTTT	AATAGGGATT	660
GCGGTTAAAA	TCCCGTCTTT	TCCCTTCACA	CATGGCTGCC	TTATGCGTAT	TCTAACGCC	720
CCACTC						726

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214

SUBSTITUTE SHEET (RULE 26)

870

AAGAGGTCTC	TTATGTTAAT	AGATATTCTC	CACATCTCTT	TTGATAGCTT	TAGTTTTGAG	60
AGCATTTTAC	CCATGCTGGT	GTTGGTGTGT	GGGGGGATTT	TCACGCTCTT	AATCAACGCT	120
TTCACTTCCA	GGTTTTTCGG	CAATTGGAAT	GTGTTTTTAT	GCATGCTCTT	TTTGGTTTTG	180
GATTTTTTAG	TGGTTTCAGG	GTTAGAAGAG	CAAGAAAACG	CCTTTTTTGG	GTTTTTAAGC	240
CTAGATACTC	TCTCGCTCAT	CTCTCAAAGC	ATTGTCTTGA	TTTCAGCTTT	TTTTCTCATT	300
TTCTTAGCCC	TTTCAAAGA	ACGCTTCAAC	GAATTTCAAA	CCGCTGAATT	TTATTCCCTA	360
TACTTGTTTA	TTGTCGCTGG	CTTTCAGTTC	ATGGTTTCAA	GCAACCAGTT	TGTGTAAATC	420
CTTATTGGGT	TAGAAACAGC	GCCTTTGCCC	CTTTGTGTGT	TAATGGCGTT	GAGCGATAAA	480
CGCTACGGCT	TAGAAGCAGG	GATCAAGTAT	TTCACCATGG	GGGCGATGGC	GAGCGCGTTT	540
TTTGCTATGG	GCGCGATGGC	TTTTTACCTG	CTTACAGGGA	GCTTGAATCT	TGAAGTCATT	600
ACCCTATACT	TACACACTGA	GGGCATCACA	AACCCCATGC	TCCTTTCGAT	GGGCACTATT	660
TTTTTGATTG	GAGCGATTGG	CTTTAAGGTT	TCCTTAGTGC	CTTTCCATAC	CTGGATGCCT	720
GATGTGTATG	AGGGCAATAA	CCCACTCTTT	GCGAGCTATA	TTTCCATTGT	GCCTAAAATC	780
GCTGGCTTTG	TGGTAGCGAC	TCGCTTTTTT	GGGGCGTTTA	TAGACACTCA	TACCGCTTGG	840
GTAGAAGACA	TTTTTTATGT	TTTGATCCTT	ATGACTATCA	CCATCCCTAA	TTTCATTGCT	900
TTATGGCAAG	AAGATGTCAA	AAGGATGCTC	GCTTATAGTT	CTATTTTCGA	TTCTGGGTTT	960
GCTTTAGCGT	GCGTGTATT	CCACACTGAA	GATAGCCAAC	AAGCGATGTT	TGTTTTATGG	1020
TTTCATGTTG	CCTTCACTTA	CATTGGGGCT	TTTGGCCTTT	TATGGCTCTT	AAAAAGCCGG	1080
GAAAAACAT	GGGATGAACG	CTACGATCAC	CCCTATTCTA	AATTCAACGG	CCTTATCAAA	1140
ACCCACCCCT	TAGTGGCGAT	CTTGGGCGCT	ATTTTTGTTT	TTGGGCTTGC	AGGGATCCCG	1200
CCTTTTAGCG	TGTTTTGGGG	GAAATTTTTA	GCCGTGAAA	GCGCGTTAGA	GAGCAATCAC	1260
ATTCCTTTAG	CGGTGGTGAT	GTTAGTTAAT	AGCGCGGTGG	CTGCGTTTTA	TTATTTCCGT	1320
TGGCTCGTGG	CGATGTTTTT	CAATAAGCCC	TTACAAACCC	AAAGCTACGC	TCAAAACGAT	1380
ATTTACACCC	AAAACGCCAC	CATGCCCAT	TATGCGGTCA	TTATGCCCAT	GGCGTTAGCG	1440
TGCTTGTCT	CTGTGTTTAT	GATGCGAGGG	CTTTTAGAGT	TTGTGGCT		1488

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215

AATCCCGCTC	TTTCCCTTCA	CACATGGCTG	CCTTATGCGT	ATTCTAACGC	CCCCACTCTA	60
GGCTCTGTCA	TGCTTTTCAGC	CTTGCTTTCT	AAAATGGGGA	CTTACGCCTT	ATTACGCTTC	120
TTGCTCCCGC	TTTTTCCTGA	ACTTTCAGAA	ATTTAATTAA	CCCCCATAGC	CATTGTGGCG	180
CTGTGCATGA	TCATTTATGG	AGGTTTCTA	GCCTACGCTC	AAAAAGATTT	AAAAACCCTC	240
ATCGCTTATA	GCTCTTCTC	GCACATGGGA	GTCGTGGTGC	TTGGGGTTTT	TTCTTTCAAT	300
GTGAAGGGG	TTTCAGGGGC	GCTGTTTATG	ATGTTTGGCG	ATGGCGTTAT	CGTCATGGGA	360
TTATTTTTC	TCGCTGGTAT	CTTGGAAGAA	CGCGCCAGCA	GTTAGAAAT	CGCTCGCTTT	420
GGATCGATCG	CTAAAGCGC	TCCTGTTTTT	GCAGCCTTTT	TTATGATCGT	TTAATGGCG	480
AATGTGGGCA	TGCTTTTAA	CATTGGTTTT	GTGGGAGAGT	TTTTGAGCTT	GTTAGGGTTT	540
TTTGCCACTT	ACCCTCTTTT	GGCTATCATT	GCCGGGACAA	GCATCATTTCT	ATCAGCGGTT	600
TACATGCTCA	CTTCATATAA	AGATGTGTTT	TTTGGAAGT	TAAAAACCGG	GAACAACCAA	660
ATCAGCGTGT	TTGAAGATTT	AAACGCTCGT	GAGGTAGGGG	TTTTAAGCGT	GATTTTAGCT	720
TTGATCTTAA	TTTTAGGGAT	TTATCCTAAA	GCGCTTTTAA	AACCGATTGA	GCAAGGCTTT	780
AAGCAGCTTT	TAGAGGTGAT	AGAAATCCGC	TCGCTCCTTT	TTTTAGGTTT	ATTGGACACT	840

SUBSTITUTE SHEET (RULE 26)

AAGATAAAAG AGGTCTCTTA TGTTAATAGA TATTCTCCAC ATCTCTTT

888

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216

ATTTATTCAA	AAACAAGGAG	TCATGACATG	GACATTAGCA	TTTTTAGAGA	ATACGATATT	60
AGAGGCATTT	ACCCCAACCAC	TTTAGATGAA	AATACGGCTT	TTAGTATCGG	CGTGGAGTTG	120
GGAAAAATCA	TGCGAGAATA	CGATAAAAGC	GTGTTTGTAG	GGCATGACGC	AAGGGTGCAT	180
GGGCGTTTTT	TGTTTGAAGT	TTTGAGCGCG	GGGCTGCAAT	CAAGCGGCTT	GAAAGTGTAT	240
GATTTAGGGC	TAATCCCCAC	ACCGGTAGCG	TATTTTGCGG	CCTTTAATGA	AATAGACAAT	300
ATCCAATGCC	CTAATCCAT	CATGATCACT	GGCTCTCACA	ACCCCAAAGA	ATACAACGGC	360
TTTAAAATCA	CGCTCAATCA	AAACCCGTTT	TATGGCAAGG	ACATTCAGGC	TTTAAAAAAC	420
ACGCTTTTAA	ACGCAAGCA	TGAAATAAAG	CCCCTAAAAG	AAACGCCAGA	GAAAGTCAAT	480
GCCCTAGAAG	CGTATCATCG	CTATTTGATC	AAGGATTTTA	AGCATTTTAA	AAATCTTAA	540
TACAAAATCG	CCCTGGATT	TGGTAATGGC	GTGGGGGCGT	TAGGATTAGA	GCCGATTTTA	600
AAGGCTTTAA	ACATTGATTT	TAGCAGCCTT	TATAGCGATC	CTGATGGGGA	TTTTCCTAAC	660
CACCACCCAG	ACCCTAGCGA	AGCGAAAAAC	TTAAAAGACT	TAGAAAAACA	CATGCGAGAA	720
AACGCTATTT	TAATAGGCTT	TGCTTTTGAT	GGCGATGCGG	ATAGGATTGC	GATGCTAAGC	780
TCTCATCATA	TCTATGCGGG	CGATGAATTA	GCGATTTTAT	TCGCTAAACG	CTTGCAATGCT	840
CAAGGCATCA	CCCCTTTGT	GATCGGCGAA	GTCAAATGCT	CTCAAGTGAT	GTATAACGCA	900
ATCAATACTT	TTGGTAAGAC	GCTCATGTAT	AAAACCGGGC	ATAGCAATTT	AAAAATCAAG	960
CTCAAAGAAA	CTAATGCGCA	TTTTGCGGCT	GAAATGAGCG	GGCATATCTT	TTTTAAAGAA	1020
CGCTATTTTG	GCTATGATGA	CGCTCTTAC	GCATGTTTAA	GGGCTTTGGA	GTTATTGCTT	1080
GAACAAAGTC	CAAGCGACTT	GGAAACACC	ATTAATAACC	TCCCCTATTC	CTACACCACG	1140
CCTGAAGAAA	AAATCGCCGT	GAGCGAAGAA	GAAAAATTTG	AAATCATTCG	CAACTTACAA	1200
GAAGCGCTTA	AAAACCCGCC	AAGCCATTTC	CCTACAATCA	AAGAAATCAT	CAGCATTGAT	1260
GGCGTGAGAG	TGGTTTTTGA	ACATGGCTTT	GGGCTTATTC	GCGCAAGCAA	CACCACCCCC	1320
TATTTAGTCA	GCCGCTTTGA	AGGCAAGGAT	GAAACACAG	CGTTAGAATA	TAAAAGGGCG	1380
TTGCTTGGGC	TATTAGAAAA	ACTT				1404

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

872

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217

GGAATTTTGA	TGAATGAGAT	CATTTTAATC	ACCGGCGCTT	ATGGCATGGT	GGGGCAGAAC	60
ACGGCGTGTG	ATTTTAAAAA	AAACAAGCCT	GATGTTACCT	TACTCACCCC	TAAAAAGAGC	120
GAATTGTATT	TGTTGGATAA	AGACAACGTT	CAAGCCTATT	TGAAAGAATA	CAAGCCTACA	180
GGCATTATCC	ATTGTGCCGG	GAGAGTGGGG	GGCATTGTGG	CAAACATGAA	CGATCTTTCA	240
ACTTACATGG	TTGAGAAATT	ACTCATGGGT	TTGTATCTTT	TTTCTAGCGC	TTTAGATTGT	300
GGCGTGAAAA	AAGCCATTAA	TCTAGCGAGC	TCTTGCGCTT	ATCCTAAATA	CGCCCCTAAC	360
CCTTTAAAG	AGAGCGATTT	ATTGAACGGC	TCTTTAGAAC	CAACGAATGA	AGGCTACGCT	420
TTAGCCAAAC	TCTCTGTGAT	GAAGTATTGC	GAATACGTGA	GCGCTGAAAA	AGGCGTTTTT	480
TATAAAACTC	TAGTGCCCTG	TAACCTTTAT	GGCGAGTTTG	ACAAGTTTGA	AGAAAAGATA	540
GCGCACATGA	TACCAGGGCT	TATTGCTAGG	ATGCACACCG	CTAAATTAAA	AAATGAAAAA	600
AATTTTGCGA	TGTGGGGCGA	TGGCACGGCC	GAAGAGAGTA	TC		642

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1215 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218

GCTCACGCCA	ACCGCACCAT	CATCCACAGG	ATTGATGATA	GCATCGCGCA	GCGCGTGGAT	60
AATGCCATTG	GCCCCATGCG	TTTGGTTAGA	GGGTTTGCCC	CCCTTTACCT	CACTTTACCC	120
AAACGCTCTT	TTAATGCGCC	CAAAAAGATT	TTAGCGCTTG	GAGCGGAGCA	AAAAGGGCAT	180
TTTAGCTTAC	TAGATAGCGA	AACTTCTGTT	CTTTTACTCT	CGCCTTTTIG	TGGGGATTG	240
AGCGTTTITAG	AAAATGAAAA	ACACTTTAAA	GAAACTTTGA	ATTTTTTCTT	AAAAACCTAT	300
GATTTCAAAC	CCACGCTCTT	AGCTTGCGAT	GAGCATCAAA	ACTACACCAC	CACCAAAATG	360
GCTTTTGATT	TTAATACGCC	CTTGTGCAA	GTCCAGCACC	ACCATGCCCA	CTTTTITAGCG	420
AGCGTCTTAG	ACGCATTATT	ACAAGATCCG	CATTTAAATC	ACCCCTTTAT	AGGTATTGTT	480
TGGGACGGGA	GTGGGGCTTA	TGAAAATAAG	ATTTATGGGG	CGGAGTGTTT	TGTGGGGGAT	540
TTGGAACGCA	TTGAAGAAGT	GGCTAGATTT	GAAGAATTTT	GGCTTTITAGG	GGGGCAAAAA	600
GCGATCAAAG	AGCCTAGAAG	ATTGGTTTAA	GAAATCGCTT	TAAAACACCA	GCTCAACAAG	660
CTTTTAAAC	GCGTTCAAAA	GCATTTCAAA	GAAGACGAAT	TAGGAATTTT	TAAACAAATG	720
CATGACAAAA	AAATTCAAAG	CGTCGCCACC	AATTCCATAG	GCGGTTTGTT	TGATATAGTG	780
GCGTTITAGT	TGGGCGTGGT	GGGAACGATT	AGTTTITGAAG	CCGAGAGCGG	GCAGGTTTTA	840
GAAAATCTAG	CCCTACAAAG	CGATGAGATC	GCTTTTTACC	CTTTTGAAAT	CAAAAACAGC	900
GTGGTGCGTT	TGAAGGAATT	TTATCAAGCG	TTTGAAAAGG	ATTTGGGCGT	TTTGAACCCC	960
AAACGCATCG	CTAAGAAATT	TTTTAACAGC	TTAGTAGAAA	TCATTACCGC	TTTGATTGCG	1020
CTTTTAAAG	GGCATGTCGT	GGTGTGCAGT	GGGGCGTGT	TTTGCAACCA	ATTGTTGTGC	1080
GAACAATTAG	CCAAGCGATT	GAAAAGCTT	CAAAGGGAGT	ATTTTTTCCA	CAAGCATTTT	1140

SUBSTITUTE SHEET (RULE 26)

873

CCCCCTAATG ACAGCAGTAT CCCTGTCGGT CAAGCCTTAA TGGCGTATTT CAACCCTACA 1200
ATCATCAAAA AAGGA 1215

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219

CGCTTTGAGT	GCGGAGCGAG	CGACATGAGC	GGGTGGCTTT	TAATGGGATT	ACCGGGAGCT	60
TTATATGTGG	GGGGGCTTAT	CAATTCACAC	ATCGCCATAG	GCTTGAGTTT	GGGCGCACTC	120
ATTAAGTGGG	TTTTTGTTGGC	TAAGCGCTTA	CGCATTATTA	CGAGCGTGAT	CGCTAATTCT	180
ATTACCAATT	CAGATTATTT	TGAAACGCGC	TTTAGCGATG	ATAAACACAT	CTTGCGCTTG	240
ATTTACAGCTT	TTGTGATTTT	AATCTTAAAG	ATTTTTTATT	TTTCTTCAGG	GCTAGTGAGT	300
GGGGCTAAAC	TCITTGAACC	GACCTTTGGC	ATTCAATACA	CCTACGCTTT	AAGCATTGGC	360
ACGCTGATTA	TTGTTTCTTA	CACCTTTTTA	GGAAGGTATA	AGGCGGTGTG	CTGGACGGAT	420
TTGATTCAAG	GGCTTTTGAT	GATGAGCGCT	TTAATCGTGG	TGCCGATCGT	TATGATAATC	480
CATCTTGGAG	GGATTGGAGA	GGGGATTAAA	ATCATTAAAG	AGATCAAGCC	TGAAAACCTT	540
TCTTTCTTGC	AAGGCTCTAG	CGTAGTCGCT	ATTATTTCAA	GCCTTGCTTG	GGGGTTAGGC	600
TATTTTGGGC	AACCCCATAT	TTTAGTGCGC	TTCATGTCTA	TCCGCTCCAT	TAGAGATGTG	660
CCTAAAGCGA	CCACTATTGG	GATTTCTTGG	ATGGTTATTT	CTTTAATTGG	GGCATGCGTT	720
ATGGGGCTTT	TAGGCGTTGC	TTATGTACAT	AAATTGACT	TGAGTTTAGA	AGACCCTGAA	780
AAGATTTTCA	TTGTAATGAG	TCAATTGCTC	TTTAACCCTT	GGATCACAGG	CATTTTATTG	840
AGCGCGATTT	TAGCGGCGGT	GATGAGCACG	GCCAGTTCGC	AACTGCTTGT	AAGCTCTTCT	900
ACCATTGCTG	AAGATTCTA	TGCGACGATT	TTCAATAAAA	ACGCCCCCCA	AAAATTAGTG	960
ATGACGATTT	CTAGGCTTTC	GGTTTAGGG	GTGGCTTGCA	TGCTTTTATT	CATTTCAACG	1020
GATAAAACG	CTAGCATCCT	CAGCATCGTG	AGTTACGCAT	GGGCTGGCTT	TGGCGCGAGT	1080
TTTGCTCTG	TGATTTTGTT	TTCACTTTTT	TGGTCAAGAA	TGACGCGCAT	TGGCGCGATT	1140
GCTGGCATGC	TCTCTGGGGC	TAGCACGGTG	ATTTTATACG	ATAAATTGG	CAAAAGCTTT	1200
TGGATATTT	ATGAAATCGT	TCCGGGCTTT	ATTGTAGCGA	GCGTAGCTAT	TGTTGCGTTT	1260
AGTTTGTTTT	CTAGCGTGCG	ATCAGGCACT	AAAGAGGCCT	TTGAAACCAT	GCTTAAAGAA	1320
ATTGAGAGCT	TAAAGCAT					1338

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

874

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220

AATAAGTGA	TTAAAGGGC	GGTTGTTTT	GTAGGGGGT	TGCAACGAT	TACAACCTTT	60
TCTTTAATCT	ACCACCAAAA	GCCAAAAGCC	CCCCTAAATA	ACCAGCCTAG	CCTTTTGAAT	120
GACGATGAGG	TGAAATACCC	CTTACAAGAC	TACACTTTCA	CTCAAAACCC	ACAGCCAACT	180
AACACGGAAA	GCTCCAAAGA	CGCTACCATC	AAAGCCTTAC	AAGAACAGCT	CAAAGCCGCT	240
TTAAAAGCCC	TAAACTCCAA	AGAAATGAAT	TATTCCAAAG	AAGAGACTTT	TACTAGCCCT	300
CCCATGGATC	CAAAAACAAC	CCCCCTAAA	AAAGACTTTT	CTCCAAAACA	ATTAGATTTA	360
CTGGCCTCTC	GCATCACCCC	TTTCAAGCAA	AGCCCTAAAA	ATTACGAAGA	AAACCTGATT	420
TTCCCTGTGG	ATAACCCTAA	TGGCATTGAT	AGTTTCACTA	ACCTTAAAGA	AAAAGACATC	480
GCCACTAATG	AAAACAAGCT	TTTACGCACC	ATTACAGCTG	ACAAAATGAT	ACCCGCTTTT	540
TTGATTACGC	CCATTTCTAG	CCAGATCGCT	GGTAAAGTGA	TGCGCAAGT	GGAGAGCGAT	600
ATTTTTGCAA	GCATGGGCAA	AGCCGTCTTA	ATCCCCAAAG	GCTCTAAAGT	CATAGGCTAT	660
TACAGCAACA	ATAACAAAAT	GGGCGAATAC	CGCTTGGATA	TGTATGGAG	TCGAATCATC	720
ACTCCCCATG	GCATTAATAT	CATGCTCACT	AACGCTAAAG	GGGCGGACAT	TAAAGGCTAT	780
AACGGCTTAG	TGGGGGAATT	GATTGAAAGG	AATTTCCAAC	GCTATGGCGT	GCCGTTACTG	840
CTTTCTACGC	TCACTAACGG	CCTATTGATT	GGGATCACTT	CGGCTTTAAA	CAACAGAGGC	900
AATAAAGAAG	AGGTGACTAA	TTTCTTTGGG	GATTATCTTT	TATTGCAATT	GATGAGGCAA	960
AGCGGCATGG	GGATCAATCA	AGTGGTCAAT	CAAATTTTAA	GAGACAAGAG	CAAGATCGCC	1020
CCCATTGTGG	TGATTAGAGA	GGGAGTAGG	GTCTTCATTT	CGCCCAATAC	TGACATCTTC	1080
TTCCCTATAC	CCAGAGAGAA	TGAAGTCATC	GCTGAGTTTT	TGAAG		1125

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221

AAAGCGCGT	TTTGTATAGG	GATTTTTTTC	TATGGCGCTT	ATTATTTCTT	AGATGAATTT	60
TTAATCAAGC	TTTATTGCA	GCCAAGCGAG	CAAGACGCGC	TCTTTATGCA	AGAGACTAAA	120
AGAGCGATGA	ATATTTATTA	TGTGGGCTAT	GTTTTTTTAG	GCATGACTTT	GTTGTGCGCG	180
GTGTTTTTCC	AATCTATTCA	ACGCACTAAA	AGTTCGTTTA	TCATCACGAT	TTCGCACACG	240
CTAGGGTTTA	TCGTTATCCT	ATTGCCGATT	TTAAGTCATT	TTTATGGGGT	TAATGGCATT	300
TGGGTAACCT	ACCCTATTGC	GCAATTTTTA	GCCGTTTTTG	GTAGCGTTAG	GGGTAACCTA	360
TTA						363

(2) INFORMATION FOR SEQ ID NO:1222:

SUBSTITUTE SHEET (RULE 26)

875

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222

ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTATTAC	60
TTTCATCCCTT TAGTTTTTC TATGATCTCA CTTTCTACTT ACTCTATGGT AGATGACATG	120
TTTGTGGGCA AAAAAGCTGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT	180
TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTTGGTTTTG GGGCAGCGAG CATGTGGGG	240
TATTTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTTTTAT	300
TTTGTCGCTC TAAGCGCCTT TATTTTGAGC ATGGCGTTAT TGCCTTTTAG CGAAAATATC	360
GCGCGTTTTT TGGGAGCAAT GACGCTTTAT	390

(2) INFORMATION FOR SEQ ID NO:1223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223

AATCATTTTA ATGGTGTGT TTTAGGGTT CAGCACCTTT TAGCGGATGT CTTTGTGGTG	60
AATGACAAAC GGCCCGTTTT AGCGATGTA GCGATGTTGA TTGGCTCGTT AGCGAATATC	120
TTTTCAATT ACTTGTTTAT TTTTGTGTTG GAAGTGGGGG TTCAAGGCAG CGCGATAGCC	180
ACCGTGATAG GGCATGCGAT AGGGGTTTTA GTCTTAATGC AGCATTTTTG GCGCAAAAAA	240
GGGCAGTTGT ATTTTATCAA ACGATTTTCT TTATCTTCAG TCATTTCCTC AGCTAAAAGC	300
GGTGTGCCTC AAAGCACGGC GGAATTTAGC GCTTCTATTA TGATTTTATT GTTTAATACC	360
GCTATCATGC ACACGGCGGG GGAAGGTTT GTGAGCATGT ATGGGATCGT TATGTATAAT	420
GCGATTATCT TTTTACGAC TTTGTTTGCG ATTTCTCAAG GCATCCAACC GATTGCAGAG	480
CTT	483

(2) INFORMATION FOR SEQ ID NO:1224:

SUBSTITUTE SHEET (RULE 26)

876

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224

TTTCTTAAACA	TTAGGGATTT	GACGATGATT	TTAGCTCTC	TTTTAGTGT	TGTAGGGATG	60
GCGGTGCTTT	TTCTTATTGC	TTGGGTGTTT	TCTGGCAATA	AAAGGGCTAT	AAATTATCGC	120
ACGATTGTCA	GCGCCTTTGT	GATTCAAGTG	GCTTTAGGGG	CGTTGGCTTT	ATATGTGCCT	180
TTGGGCAGAG	AAATACTGCA	GGGTTTAGCT	AGCGGCATAC	AAAGCGTGAT	TGGTTACGGC	240
TATGAGGGGG	TACGCTTTTT	ATTTGGCAAT	CTCGCTCCAA	ACGCTAAGGG	CGATCAAGGG	300
ATAGGAGGCT	TTATCTTTGC	GATCAACGTT	TTAGCGATCA	TTATCTTTTT	TGCTAGCTTG	360
ATTTCACTTC	TATATTATTT	AAAAATCATG	CCTTTAGTGA	TCAACCTCAT	CGGCGGGGCG	420
TTGCAAAAAT	GCTTAGGCAC	TTCTAAAGCA	GAAAGCATGA	GCGCAGCGGC	TAATATTTTT	480
GTGGCGCACA	CCGAAGCGCC	CTTAGTCATT	AAACCTATT	TGAAAAGCAT	GAGCGATTCA	540
GAGATTTTTG	CGGTCACTGT	CGTGGGCATG	GCTAGCGTTG	CGGGGCCTGT	GTTAGCCGGG	600
TATGCGAGCA	TGGGCATTCC	TTTACCTTAT	TTAATCGCCG	CATCGTTTAT	GTCCGCTCCT	660
GGGGGGTTGT	TGTTGCTTAA	AATCATTTAC	CCGCAAAACG	AAACCATTTT	TAGCCATGCA	720
GATGTTTCTG	CAGAAGAGCA	TGTCAATATT	ATAGAAGCTA	TCGCTAATGG	GGCAAGCACA	780
GGGCTTCATT	TAGCCTTGCA	TGTGGGGGCG	ATGCTTTTAG	CCTTTGTGGG	GATGCTCGCG	840
CTCGTTAACG	GGCTTTTAGG	GGTTGTAGGG	GGATTTTATG	GCATGGAGCA	TTTGTCTTTA	900
GGGGTGTTT	TAGGCACGCT	TTTAAACCTT	TTGGCCTTTA	TGTTAGGCGT	TCCTTGGAGC	960
CAAGCCGGGA	TTGCCGGGGA	AATCATAGGC	ATTAATAATCG	CGCTCAATGA	ATTTGTGGGC	1020
TATATGCAAT	TATTGCCTTA	TTTGGGCGAT	AACCTCCTT	TAATCTTGAG	CGAGAAAACC	1080
AAAGCGATCA	TCACCTTTGC	GTTGTGCGGA	TTGCTAACT	TAAGTTCAGT	CGCCATGCTC	1140
ATTGGGGGGC	TTGGCAGTTT	AGTGCCTAAA	AAGAAAGATT	TCATTGCCAG	GCTTGCTTTA	1200
AAAGCGGTGC	TTGTAGGCAC	GCTTTCTAAT	TTCATGAGCG	CGACTATCGC	CGGGTTATTC	1260
ATAGGGTTAA	GCGCCAAT					1278

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

877

(B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225

ACGCTATCCA	AAGAAGAGGG	ATTGATGCCA	CAAAACCAGC	TTGTGATCAC	CATCATTGAT	60
GAATCAGGCT	CTAAGCAACT	CAAATTTTCT	AAAAATTAA	AACGCAACCT	CATCATTCT	120
GTGTGATTC	TTTATTGAT	CGTGGGCTT	GGCGTGGGT	TTTTAAAT	TTAATCGCT	180
AAAATGGATA	CGATGACAAG	CGAGAGGAAT	GCGGTTTAA	GGGATTTAG	GGGTTTGAT	240
CAAAAAAATT	ACGCCCTAGC	GAAAGAGATT	AAAAACAAGC	GAGAAGAGCT	TTTATTGTG	300
GGGCAAAAGA	TCCGTGGCT	AGAATCCTTG	ATTGAAATCA	AAAAGGGGCG	TAATGGGGGA	360
GGGCATCTCT	ATGATGAAGT	GGATTTAGAA	AATTTGAGCT	TAAATCAAAA	ACATTTAGCA	420
CTCATGCTCA	TTCCTAATGG	CATGCCCTTA	AAAACCTATA	GCGCTATCAA	ACCCACTAAA	480
GAAAGGAACC	ACCCCATTA	AAAGATTAA	GGCGTTGAAT	CCGGGATCGA	TTTATCGCG	540
CCATTGAACA	CGCCTGTGTA	TGCGAGCGCT	GATGGGATTG	TGGATTTTGT	GAAGACTCGT	600
TCTAATGCGG	GGTATGGGAA	CTTGGTGCGC	ATTGAACATG	CGTTTGGTTT	CAGCTCCATT	660
TATACGCACT	TAGATCATGT	CAATGTGCAG	CCTAAAAGCT	TCATCAAAA	AGGGCAGTTG	720
ATTGGCTATA	GCGGGAAGAG	CGGTAATAGC	GGCGGCGAAA	AATTGCATTA	TGAAGTGGG	780
TTTTTGGGTA	AAATTTTAGA	CGCAGAAAA	TTCTAGCAT	GGGATTTGGA	TCATTTTCAA	840
AGCGCTTTAG	AAGAAAAATA	ATTATTGAA	TGGAAGAATC	TGTTTGGGT	TTTAGAAGAC	900
ATCGTCCAGC	TCCAAGAGCA	TGTGGATAAA	GACACCTTAA	AAGGTCAG		948

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226

GGGTTTTTGG	TGTTTTTAGA	CAGGCGTTTG	ATTGTGATGG	TTACGGACTC	TAAAGGGAGT	60
CGTTATATTA	ATGTGCATAT	CTTATTCGCG	CAAATCAGTT	TGTATGCGCT	GTTGAGCGTT	120
GTGGGATCTT	TATTGTTTTT	AGGCGTTTCA	TTACTGGTTT	TAAATAAAGA	AATTA AAAAC	180
ATTGAAAAAC	AGCATGCTTT	AATCACTAAG	GAATTTGAGA	AAAAAAGAGA	GACGAATGAA	240
AAGCTTTCTT	TGCAAAATGGA	TGAGTTTTTA	GACGATTTGC	AACTTTTCAGG	GGAGCGCATC	300
AACGATTTAG	AAGAAGTGGT	GGGGGTGAAT	AGGCCTGAAG	AAGAAAAAGA	AGAGGGCAAT	360
TTTTCCAGCC	GCTTGGATGT	GGCTGGGATT	ACCGGGCTTC	AAAAAAGCTT	TATCATGCGC	420
CTTATCCCTA	ATGACTACCC	GCTAGAATCC	TATCGGCGCG	TTTCAGCCGC	TTTAAATAAA	480
AGAATGCACC	CTATTTTGCA	TGTGTTGCAC	AACCATACCG	GGCTTGATTT	AAGCACCCT	540
ATTAACACGC	CTGTGTATGC	GAGCGCGAGC	GGGCTAGTGG	GGTTAGCGAG	CAAGGGGTGG	600
AATGGGGGGT	ATGGGAATTT	GATTAAGGTT	TTCCACCCTT	TTGGTTTTAA	AACCTACTAC	660
GCCCATTTGA	ATAAAATCGT	CGTAAAAACG	GGCGAATTTG	TCAAAAAAGG	GCAAGTTGATT	720
GGGTATAGTG	GTAATACAGG	AATGAGCACA	GGACCGCATT	TGCATTATGA	AGTGCGCTTC	780
TTAGATCAAC	CCATAAACCC	CATGAGTTTC	ACCAAATGGA	ACATGAAAGA	TTTTGAAGAA	840
GTTTTTAATA	AAGAAAGGAG	CATCAGATGG	CAATCTTTGA	TAACAATAAT	AAATCGGCTA	900
ATGCAAAAAC	AGGACCAGCG	ACTATCATCG	CTCAAGGCAC	CAAAA		945

(2) INFORMATION FOR SEQ ID NO:1227:

SUBSTITUTE SHEET (RULE 26)

878

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1380
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227

GATATTGAAT	TCGCCAATCT	TTATCATATT	CCTATTAAAG	TGATCACGCA	AAGCCCTCAA	60
AATTTGCCCC	ACACCAAAGA	AGAGATTTTA	AAAAATAGCG	GGGAGTGGAG	CGATCTTTCT	120
AGCTCACTGG	CCAGAAAAAA	AATCCTCCCT	TATTTTGACA	AAGAAAATCT	CGGTAAAAGG	180
GTCATCAACT	ACCGCTTGCA	AAATTGGGGG	GTGAGCCGTC	AAAGGTATTG	GGGAGCGCCC	240
ATTCCTATGA	TTCATTGCAA	ACATTGCGGA	ATCGTGCCCTG	AAACCCAACT	GCCGGTAACT	300
TTACCTGAAG	ACATTGTGAT	TGATGGGGAA	GGCAATCCAT	TAAAAAAGCA	TGCGAGTTGG	360
AGATTCGCTC	AATGCCCCAG	ATGCCATAAA	GACGCTTTAG	TAGAAACAGA	CACCATGGAC	420
ACTTTTATCC	AATCCAGCTG	GTATTTCTTG	CGTTATACCA	CCCCCAAAA	TCAGCGTGAA	480
AATCAAGCGT	TTGATCAAAA	TTACTTGAAG	TATTTTCATG	CGGTGGACAC	TTATATTGGC	540
GGCATTGAAC	ATGCGATTTT	GCACTTGTTA	TACGCGCGCT	TTTTCACTAA	GGCTTTAAGG	600
GATTTGGGCT	ATCTTCATTT	AGATGAGCCT	TTCAAACAGC	TTATCACTCA	AGGCATGGTC	660
TTAAAAGATG	GTGCTAAGAT	GAGCAAATCT	AAAGGCAATG	TCGTTAGCCC	TAAAGAGATA	720
CTCAAAAAAT	ACGGGGCTGA	TGCCGTAAAG	CTCTTTATCC	TTTTTGCTGC	CCCGCCGGCT	780
AAAGAATTGG	AATGGAAATG	CAACGCTTTA	GAAGGCGCGC	ACCGGTTTAT	CAAGCGCTTA	840
TACGATAAAG	CGAACGCCAT	TACCCCTACC	ACTTCTAAGC	CTGAATTTAA	AGAAGTTGGC	900
CTGAATGAAG	CGCAAAAATT	AGCCCGCAAA	AAAGTCTATG	AGGCGTTGAA	AAAATCGCAT	960
GAGATTTTCA	ATAAGGCTGA	AAGCGCTTAC	GCGTTTAACA	CTTTGATCGC	AAGCTGCATG	1020
GAGGCTTTAA	ACGCTTTGAA	CGCGCAAAGT	GATGAGCAAA	TTTTATGCGA	GGGTTATTTT	1080
GTGTTGTGTC	AAATCTTAGA	GCCTATGATC	CCGCACACGG	CATGGGAATT	GAGCGAGAGG	1140
CTTTTTTAAA	GAGAGAATTT	CAAGCCTATA	GAAGTAGATG	AAAGCGCTTT	GATAGAAGAC	1200
TTTATGACTT	TAGGGCTTAC	CATTAATGGC	AAAAGGCGCG	CGGAATTGAA	AGTCAATATT	1260
AACGCTAGCA	AAGAAGAGAT	TATTATTTTG	GCTAAAAAAG	AATTAGAGAA	ATATTTAGAA	1320
AACGCGAGCG	TTAAAAAAGA	AATTTATGTG	CCTAATAAAC	TTGTTAATTT	TGTTACCGCA	1380

(2) INFORMATION FOR SEQ ID NO:1228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

(B) LOCATION 1...1209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228

CTAAATTTGT	GGCTCAAATC	GCTTATGAGG	GGAAATTCAA	TAATGAAAAA	TAGTCATGGG	60
TTAAAGGCGT	TTTTAGAAAC	AAAGCCTAAG	GAATACCATA	AGTTCGACCC	TAGCCGTTTC	120
ATTCAAATTT	ATAAGGATTT	TAAAAACGCT	TTTTTTGAGA	TTCAAGCCAA	AGTCATTCAT	180
GTGGTAGGGA	CTAATGGTAA	GGGCAGCACA	GGGCGGTTTT	TAACCCTTTT	ATTAGCCGAT	240
CAAGGGTTTA	AAGTGTGCA	TTTCACCTCC	CCTCATGTTT	TTGAATTCAG	GGAGCGCTTT	300
TATTTGAATG	GCTCTGTTGT	TAAAGAAAGC	GTTTTAGAAA	ACGCCCACCA	GCAATTGCAA	360
TCGCACGCTT	TCAGTAACGC	TTGCTCGTAT	TTTGAATACG	CTACCTTATT	AGCTGTCATG	420
CTCGCTAAAG	ATTGCGATTA	TTTGTTTATA	GAAGCAGGGC	TTGGGGGGGA	GTTTGACAGC	480
ACGAACGCTT	TGGAAAAAAC	CCTAAGCGTT	TTCACCCCCA	TTGATTACGA	TCATAAGGAA	540
TTTTTAGGGG	ATAGTTTTAG	AAGCATTGCG	ACTACTAAAT	TAAAAGCGAT	GGGCTCTCTT	600
AATATCATCG	CTCCCCAACA	AGAACTGGTT	TAAATGTGG	CTCAAAAAAT	CGCTAAAGAC	660
AAACACGCCG	AATTGATTGT	GGTTCAAAAT	GAAATTTCAA	AAGGAGTGAG	CGATTATATT	720
GAACGCCACC	ATTAGCCCCA	TTTTTTAGCG	ATGAATTTAG	AAGTGGCTCT	AAAGGCGTTT	780
GAAACGCTAT	TGCCATGCAA	TAAACAAGAA	GTTTTAAAAA	ACCTAAAGCC	CCTAGATTTA	840
ATCGGCCGTT	GCGAGCTTTT	AAGCCCTAAC	ATTTTAATAG	ATGTGGGGCA	TAACCCCCAT	900
AGCGCTAAAG	CCTTAAAAGA	AGAAATCAAA	CGCATCTTTA	ACGCTCCAAT	CGTTTTGATT	960
TATAATTGCT	ATCAAGATAA	AGACGCTTTT	TTGGTGCTAG	AAATTTTAAA	GTCTGTGGTT	1020
AAAAAGGTTT	TGATTTTAGA	ATTGCATAAT	GAAAGAATTA	TCCAATTAGA	AAACTTTAAA	1080
GGGATTTTAG	AAACTTTAGG	GTTAGAACAC	GCCTTGTTTG	AAGAAGTGAA	AGAAAATGAA	1140
AATTATTTGG	TGTATGGCTC	ATTTCTGGTA	GCCAACGCTT	TTTATGAACG	CTATCCAAAG	1200
AAGAGGGAT						1209

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229

AGCGTGTTCA	GTCATAGCGG	GAGCGCGGAT	TTGTTGGAAA	ATTTGGGCGT	GAATATTGAA	60
ATGAACCCCA	TGCAATTAGA	AAATTGCTTC	AAACAATCGC	ATTTTGGGTT	TTTATTCGCG	120
CCTTTATACC	ATCAAAGTTT	TAAAAAATCC	GCCCCTTTAA	GAAAAGAGCT	TTTCACTAAA	180
ACGATTTTCA	ATTGCTTAGG	GCCTTTAATC	AACCCCTTAA	GGCCAAAAAT	CCAGCTTTTA	240
GGCGTGTATG	ACAAATCCTT	GTGTAAGACC	ATGGCGCTAG	CGTTGAAGGC	TTTAGGCGTT	300
AAAAGGGCGA	TGGTGGTTAA	TGGAGGGGGG	ACAGATGAAA	TCGTGTTGCA	TGACATTACG	360
CATGCGTGCG	AATTGAAAAA	TAACGAAATT	TTAGAGTATG	ATTTGAGCGC	TAAAGATTTT	420
GATTTACCCC	CCTATGATTT	GAAAGAATTA	CAGATTGAAA	ACGCCAAAGA	AAGCGTTCAA	480
GCGTGTTTAG	ATATTTTAGA	AAATAAAGGC	AAAGATTCCG	ATACAATGGT	GGTTGCGGCG	540
AATGTGGCGA	GTTTGTGTGA	TTGAGCCCAT	AGGGCTAAAG	GATTTAAAAG	AGGGCGTGAG	600
CATGACTTTA	GAGCATTTAA	AAACCAAAGC	GCATTATGTG	CATTTACAAA	AAATCATAAG	660
GCTAAGCCAT	GCCTAGCGTG	T				681

(2) INFORMATION FOR SEQ ID NO:1230:

SUBSTITUTE SHEET (RULE 26)

880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230

AATTTGGTAG	TGAGTGTTC	TGCAACGAGT	GCGAATTTAG	GCCCCGGTTT	TGATTGCTTG	60
GGTTTGAGTT	TGAATTTACG	CAATCGTTTT	TTTATTGAGC	CTAGTAATAT	CCATGCGGTG	120
AAATTGGTTG	GGGAGGGTGA	AGGGATCCCT	AAATTTTTAA	CCAACAATAT	TTTCACCAAA	180
GTGTTTATG	AGATTTTAAA	AAAGCATGGG	AATGACGGCT	CGTTTAAATT	TTTATTGCAT	240
AATAAAGTCC	CTATTACAAG	GGGCATGGGG	TCTAGCTCAG	CGATGATTGT	GGGGGCGGTC	300
GCTTCAGCGT	TGCGGTTTTT	AGGGTTTGCT	TTTGATAGAG	AAAACATTCT	CAATACTGCT	360
CTAATTTATG	AAAACCACCC	GGATAATATC	ACCCCGGCGG	TGTTTGGGGG	GTATAATGCA	420
GCGTTTGTGG	AAAAAAAGAA	AGTGATAAGT	TTAAAAACCA	AAATCCCTTC	TTTTTTAAAA	480
GCGGTGATGG	TGATCCCTAA	TAGGGTCATT	TCTACCAAGC	AATCGCGCCA	TCTCTTGCCC	540
AAGCGTTACA	GCGTGCAAGA	AAGCGTGTTT	AACCTTTCGC	ATGCGAGTTT	GATGACGATG	600
GCGATTGTGC	AAGGGAAGTG	GGACTTGTTG	CGTTGTGTTT	CTAAAGACAG	GATGCACCAA	660
TATAAGCGCA	TGCAAACTTA	TCCCGTGTG	TTTGCGATCC	AAAAGCTCGC	TTTAGAAAAT	720
AACGCCCTTA	TGAGCACGCT	TTCAGGGAGT	GGTTCGTCGT	TTTTTAACAT	GTGTTATGAA	780
GAAGACGCTC	CTAAATTAAA	GCAGGTTTGG	AGCAAGAAAT	TCCCTAAATT	TAGGGTAGCG	840
GTTTTAGATT	TTGACAATGA	TGGAGTCCTT	ATTGAGAAAG	AC		882

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231

TTAGTATTCA	AAAAGCCCTT	TTTTAAAAAT	AGGTTACTAA	ACGTTACTAA	TAAGTTAAAA	60
TTCGTGAAAA	TAACCATAAT	GATTAAAGAT	TTTAACCACT	ATTGTAGAAA	AATAACGAGA	120
GGGTTTGTAA	AAATTCCAC	CAAAAAACAA	GGAGCAAAAA	AGATGAAAAA	AGCGGGTTT	180

SUBSTITUTE SHEET (RULE 26)

881

CTTTTTTGG	CGGCGATGGC	TATCATTGTT	GTGAGTTTAA	ACGCCAAAGA	TCCGAATGTC	240
TTGCGTAAGA	TTGTTTTTGA	GAAATGTTTG	CCTAATTATG	AGAAAAATCA	AAATCCTTCA	300
CCATGCATAG	AAGTCAAACC	CGACGCCGGC	TATGTGGTTT	TAAAAGATAT	TAACGGTCCG	360
TTGCAATATT	TGTTGATGCC	AACGACTCAC	ATTAGTGGCA	TGAAAACCC	TTTGTGCTT	420
GATCCTTCTA	CGCCTAACIT	TTTTTACTTG	TCATGGCAAG	CGCGCGATT	TATGAGTAAA	480
AAATACGGAA	AACCCATTCC	TGATTATGCG	ATCTCTTTGA	CGATCAATTC	TAAAAAAGGG	540
CGATCGCAAA	ACCATTTTCA	CATCCATATT	TCTTGCATTA	GCCTTGATGT	GCGCAAACAG	600
CTGGATAATA	ATCTAAAAAA	TATCAACAGC	CGTTGGTCGC	CATTATCAGG	TGGCTTGAAC	660
GGGCATAAAT	ATTGGCGCGC	TCGGGTAACA	GAGAGCGAAT	TAGCGCAAAA	AAGCCCGTTT	720
GTTCATGCTTG	CTAAAGAAGT	GCCTAACGCG	CACAAACGCA	TGGGAGACTA	TGGCTTGGCG	780
GTGGTGCAAC	AGAGCGATAA	CTCCTTTGTC	TTGTTAGCGA	CACAATTTAA	CCCATTGACT	840
TTAAATCGCG	CTTCAGCCGA	AGAGATTCAA	GATCATGAAT	GCGCGATTTT	GCGT	894

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232

TATCATCGCA	CTAATACCAC	GATAAGGATA	ATTATCATGC	AAGATTTACC	CCCATGCCCT	60
AAACGCAACG	ACGCCTACAC	CTACCATGAT	GGCAGCGAGT	TCGTTTGCTC	TAGCTGTTTG	120
TATGAATGGA	ATGGAAATGA	AATTAGTAAT	GAAGAATTGA	TCGTTAAAGA	TTGCCATAAT	180
AATCTTTTAC	AAAATGGGGA	CTCGGTCATT	CTCATTAAAG	ATTTAAAGGT	TAAAGGCTCA	240
TCTTTGGTGC	TTAAAAAAGG	CACTAAAAATC	AAAAATATCA	AGCTTGCTCA	TAGCGATCAC	300
AATGTGGATT	GTAAGTGGA	AGGGCAGAGC	TTGTCTTTAA	AATCTGAATT	CCTTAAAAAA	360
GCT						363

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

882

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233

AAGGGTTGTT	TTATGCGAGA	ATTTTTTAAG	AAACTTGGCA	CAGAATACGC	TTCCAAGCTG	60
TTTTTGGTTT	ATTGGCTTAG	ATGGATGTTG	AGTGCCTTGG	TGATGCTGCC	TTTTATGGAG	120
GTTTTTTATT	ATTTCAATTT	TCCGTTGTGG	CTCAATCTTT	TCTTAGGGCA	AACCATTGGA	180
GCGGTGATTT	TTTTCAAGTT	GGATAAGTTG	ATTTTTTCTA	AAAAA		225

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234

TTCTTTAAAC	GCTATGAAAG	GTTAAGCATG	CAATATTCCT	CTTTGCTGTC	AGTGGTGTTG	60
TTTTTGCCCT	TAATCGGTGC	GGTTTATGCG	GGGCTGTTTG	GGGCTAAAGC	TAAAGCGTTG	120
CATGTGGGCG	TTTTCAATTC	TTTGTGCGTG	CTGGTTTCCT	TCATTGGCGC	GGTGGTTCTT	180
TTCAATCAAG	CATGGCATCA	TCAAAGCTAT	GAAAAATATT	TGTTTGACTG	GATCGTGGA	240
GGGAATTTTA	AAGTCGGCTT	TTCCCTCATG	CTGGATAATA	TCAATGCGGT	CATGATTGTC	300
GTGGTCACTC	TAGTTTCTTT	CTTAGTGCA	GTGTATTCTA	TAGGCTATAT	GGAGCATGAT	360
ACAGGGTTTA	ACCGCTATTT	TTCTACCTT	AGCGGCTTTG	TGTTTTCCAT	GCTGGTGTTG	420
GTGTTGAGCG	ATAATTTTTT	AGGGCTTTTC	ATTGGCTGGG	AAGGGGTGGG	GCTATGCTCT	480
TACTTGCTCA	TTGGCTTTTG	GTATCATAAA	AAAAGCGCGA	ATAACGCTTC	TATTGAAGCC	540
TTTGTGATGA	ATCGAATCAC	GGATTTAGGC	ATGCTCATGG	GGATTATTTT	GATCTTTTGG	600
AATTTTGGCA	CCCTCCAGTA	TAAAGAAGTC	TTTAGCATGC	TCAATAACGC	CGATTATTCC	660
ATGCTCTTTT	ACATTAGCGT	GTTTCTTTTT	ATTGGCGCTA	TGGGGAAGAG	TGCTCAATTC	720
CCTATGCACA	CATGGTTAGC	CAACGCTATG	GAGGGGCCTA	CCCCGTGATC	CGCTCTCATC	780
CATGCAGCGA	CGATGGTAAC	CGCTGGGGTG	TATCTAATCA	TCAGAGCCAA	TCCTTTGTAT	840
AGTGGCGGTG	TTGAAGTGGG	TTATTTTATC	GCATGCTTAG	GAGCGTTTGT	GGCTCTTTTT	900
GGAGCGAGCA	TGGCTTTAGT	CAATAAGGAT	TTAAAACGCA	TCGTGGCTTA	TTCCACGCTT	960
TCTCAATTAG	GCTATATGTT	TGTAGCGGCC	GGGCTTGGGG	CTTATGCGAT	CGCGCTTTTC	1020
CACCTCTTTA	CGCATGCGTT	CTTCAAATCC	CTCCTTTTCT	TAGGCTCAGG	CAATGTCATG	1080
CATGCGATGG	AAGACAATCT	GGATATTACT	AAAATGGGCG	CTTTATACAA	GCCTATGAGG	1140
ATCAGAGCTG	TCTTTATGAT	TATAGGGTCA	GTGGCTTTGT	GTGGGATCTA	CCCCTTTGCG	1200
GGCTATTTCT	CCAAAGACAA	GATTTTAGAG	GTGCGCTTTG	GGATGCACCA	CCACATTTTA	1260
TGGTTTGTTT	TTTTGATTGG	GGCGATCTTT	ACCGCTTTTT	ATAGCTTCAG	ACTCATCATG	1320
CTGGTGTTTT	TTGCACCCAA	ACAACATGAA	ATCAACCACC	CCCATGAAGG	CCAAAAATTT	1380
CATGCTTTTG	AGCATGCTAC	CGTTAGGGGT	TTTGGCGGTC	ATTGCCGGTT	TTTCAGAAGA	1440
GCCGTTTTTT	CATTTTATCT	CTCAAGTGAA	TTCTAGTGT	TGGAGACTAT	C	1491

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

883

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235

AACAAGCCGA	ACAAGGGTGC	AGTATTGGAG	AAAACAAAGA	AGAGGCAGTT	GCTTCAAAAG	60
AAAACAAAGA	AGAGAATAAA	ACAGAAGCCG	CTGCCCCAAA	AGAAAATCAA	ACAGAAAACA	120
AGACAGAGGT	TAAAGAGAAA	AATTGAAGTC	CCTACCAAAA	CCACTTACTT	GTTGCTTGAA	180
GAAGCGGGCA	TCAATTTAGA	AACTTATGAA	AAAATTCTCG	CTCTTTTGCA	AAAATCAAAT	240
AACACCTTGC	TAGTGGTTGG	CGAGGAAATT	TATAGCCACA	AACAAGCCCCA	TAACATCGCT	300
AAAATGTTGC	GTTTATTAGC	CCAAAAAGC	GCTATTAAAC	TCATTCTTAT	CCCCCAAGC	360
GCGAACGCCT	TAGGCATCGC	TTCTATTTGC	GAATTGAGCG	AAGAAGTTTT	TGAACATGAA	420
AAAATCGTAG	GCAITTCGCG	TCAAGGGGAT	TTCACATATCA	ATAGCGACGA	TAGGGTTTTT	480
GGGAAAGACG	CTGTCACTAA	AGTGGATTTT	ATTCTGCCCA	GTCTCAACCA	ACTAGAAGGC	540
ACGATCACTA	ATGTTGAAGG	CGGTGTGTTG	CCCTTAAAC	CGGCTTTAAG	GTTTGAAGGC	600
TATGACTTGA	CGCATATCAT	GCAAGGCTTT	GGCTTTGTGG	AAGAAAACCT	CACAGAATGC	660
ACCCACAAAC	TCCCTACAGA	AGCGGGCTTT	AAAGCCTTAG	AGTTTGATCA	TCTAACCAAC	720
TATTTCATA	ACGACAGGGC	TAATCACAGA	GGCTATTTAT	TAGGAACAAG	CCATTTTGAA	780
AATAGCGCTA	AAGAATCGAA	GCCACAGAAT	GCGAGCCTAT	CAAGCCTT		828

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 669 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236

GGAGGTTTTA	TGGCCAAACA	AGAATACAAG	CAACTTCCTA	AACGAGCCGA	AGTCCATAGC	60
GCGACCGAGC	AGTTTAAAGA	CACCATTAAG	ACGAGCTTGG	GTTTGGATCT	ATTCAAAGGG	120
TTAGGGGCTA	CGATCAAGGA	ATTTTATTAG	CCAAGCGTAA	CCATCCATTA	CCCTATGGAG	180
CAACTCCCTT	TAAGCCCACG	CTATCGCGCG	GTGCATCATT	TGCAACGGCT	TTTAGACTCA	240
GGCTCTGAAA	GGTGATATAG	CTGTGGGCTG	TGCGAAAAGA	TTGCACGAG	CAACTGCATA	300
AGGATCATCA	CGCATAAGGG	CGAAGACAAC	CGCAAAAAGA	TCGATTCTTA	CACGATCAAT	360
TTGGGGCGTT	GCATTATTG	CGGTTGTGT	GCGGAAGTTT	GCCAGAATT	GGCGATCGTT	420
ATGGGGAATC	GTTTGAATAA	CGCCAGCACC	CAACGCTCCC	AATACGGCTC	TAAAAGCGAG	480

SUBSTITUTE SHEET (RULE 26)

884

TTTCTAACGA	GCGAACAAGA	CGCTAAAAAC	TGCTCGCATG	CCGAATTTTT	AGGCTTTGGT	540
GCGGTAAGCC	CTAATTATAA	CGAACGCATG	CAAGCCACCC	CTTTAGATTA	TGTCCAAGAA	600
CCTTCAAAG	AAGAATCCAA	AGAAGAGTCT	CCAACAAGCC	CAGAAAGCCA	TAAGGGAGAT	660
GAAAATGTT						669

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237

ATTATGTCCA	AGAACCTTCA	AAAGAAGAAT	CCAAAGAAGA	GTCTCCAACA	AGCCCAGAAA	60
GCCATAAGGG	AGATGAAAAT	GTTTGAAACC	ATTGCCTTTT	ATTTCTTTGC	GATCCTTACT	120
TTAAGCATGG	CGTTAGTGGT	GATCACAACC	ACAAATATCC	TCTATGCCAT	TACCGCTCTC	180
GCTAGTAGCA	TGGTTTTTAT	TTCTGCTTTT	TTCTTTTAC	TGGACGCTGA	GTTTTTGGGC	240
GTGGTGCAAA	TCACGGTGTA	TGTGGGTGCG	GTCAATGTGA	TGTATGCGTT	TGGCATGATG	300
TTTTTCAACT	CCGCTGCAGA	AGTAGTTGAA	CGCAAGCAAA	GCCCTAAAAT	CTTGTGCGTT	360
CTTTCATTG	GCGTGCGCT	GTTGCTCACC	TTGATTTTAA	GCGCTCCTAG	CATTGGCGAA	420
AACCTTTCTA	AGCAAGTCAA	TTCCAACGCT	ATTGATGCGC	AAATCCCTAA	CATTAAAGCG	480
ATTGTTATG	TGCTTTTCAC	CAATTACCTC	ATTCCCTTTG	AAGCGGCGGC	TTTAATGCTT	540
TTAGTCGCTA	TGGTTGGAGG	CATCGCTACA	GGGATTCAAA	AAATCCATGG	GAAAAATCAC	600
ACGCAATTTA	TAAAGGAATC	TCTA				624

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238

SUBSTITUTE SHEET (RULE 26)

885

ATGAAACAAT	TTAAAAAGAA	ACCAAAAAAG	ATAAAACGAT	CGCATCAAAA	TCAAAAAACA	60
ATCTTAAAGC	GTCCTTTATG	GCTTATGCCT	TTACTGATTG	GCGGGTTTGC	TAGTGGGGTG	120
TATGCCGGATG	GAACAGACAT	TTTGGGGCTT	AGTTGGGGGG	AAAAAAGCCA	AAAGGTATGC	180
GTGCATCGTC	CATGGTATGC	TATATGGAGT	TGGGATAAAT	GGGAGGAAAA	AACACAACAA	240
TTTACAGGAA	ACCAACTCAT	CACAAAAACT	TGGCAGGGG	GTAATGCGGC	TAACTACTAC	300
CACTCTCAAA	ACAACCAAGA	CATCACAGCC	AATTTAAAAA	ATGATAACGG	CACTTATTTT	360
TTAAGCGGTC	TGTATAACTA	CACCGGAGGG	GAATATAATG	GGGGGAATTT	AGACATTGAA	420
TTAGGCAGTA	ACGCTACTTT	TAATCTAGGT	GCGAGTAGTG	GGAATAGCTT	CACTTCTTGG	480
TATCCTAATG	GGCATACTGA	TGTTACTTTT	AGCGCTGGGA	CTATCAATGT	GAATAACAGC	540
GTAGAAGTGG	GCAATCGTGT	GGGATCGGGA	GCTGGCACGC	ACACCGGCAC	AGCCACTTTA	600
AACTTGAACG	CTAATAAGGT	TACTATCAAT	TCCAATATCA	GCGCGTATAA	AACTTCGCAA	660
GTGAATGTAG	GCAATGCTAA	CAGCGTTATT	ACCATTAAAT	CGGTTTCTTT	AAATGGGGAA	720
TACTTGCAGT	TCTTTAGC					738

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239

GTITTCACGC	CAAGGGTGAA	GCGCTTTTTC	ATCTTCTTAT	TCCTCTTTTT	AATCTTGCAT	60
GAAATCTTAA	ACACAGAATT	AGCCCTTTTA	AATGGGATTT	CGCTCGCGCT	GGGCTATTTG	120
TGTTTGTTCA	TACTCGTTTT	GAGCGCTTCT	TTAATCTTTG	AAAAAGTCTT	ATCCAAGCAG	180
TATTTGCAAA	CCGCTAAAGA	TAAATCGCC	TCTTTAAAAA	ATTTAAAAGT	CATCGCCATT	240
ACAGGAAGCT	TTGGGAAAAC	CAGCACCAAA	AATTTCTTGC	ATCAAATCTT	ACAAACCCAA	300
TTCAACGCGC	ATGCAAGCCC	TAAAGTGTC	AACACCCCTT	TAGGCATTGC	GAACGATATT	360
AACCAGAATT	TAGACGACAG	GAGTGAAATT	TATATCGCTG	AAGCTGGGGC	AAGGAATAAG	420
GGCGATATTA	AAGAAATCAC	CCGTCTCATT	GAACCGCACC	TTGCCGTGGT	CGCAGAAGTG	480
GGCGAACAGC	ATTTAGAATA	TTTTAAAACT	TTAGAAAATA	TTTGCAGAGC	TAAAGCGGAA	540
TTATTGGATT	CCAAACGCTT	AGAAAAAGCC	TTTTGCTACT	CTGTGGAAAA	AATCAAACCC	600
TATGCCCCCTA	AAGATAGCCC	TTTAATAGAC	TATTCTAGCC	TAGTTAGAAA	CGTCCAATCC	660
ACTTTAAAAAG	GCACCTCTTT	TGAAACGCTT	ATCAATGGCG	TTTGGGAAAG	CTTTGAAACG	720
AAGGTTTTTAG	GGGAGTTTAA	CGCCTATAAT	ATCGCTTCAG	CGATTTTAAAT	CGCTAAGCAT	780
TTAGGCTTAG	AGACAGAAAG	GATCAAACGG	CTTGTTTTTG	AGCTTAAGCC	TATTAACCAT	840
CGTTTGCAAC	TGTTGGAAGC	GAATCAAAAA	ATCATTATAG	ACGATAGCTT	TAATGGGAAT	900
TTAAAGGGCA	TGTTAGAGGG	CATTCGTTTA	GCGAGCTTGC	ATCAAGGGCG	TAAGGTCATT	960
GTAACACCGG	GATTAGTGGA	AAGCAATACA	GAAAGTAATG	AGGCTTTAGC	GCAAAAAATA	1020
GACGGGGTTT	TTGATGTCGC	TATCATCACA	GGGGAGTTGA	ATTCCAAAAC	GATTGCTTCC	1080
AAATTGAAAA	CCCCCAAAA	AATCTTACTC	AAGGATAAGG	CGCAATTGGA	AAATATCTTA	1140
CAAGCCACCA	CGATTCAAGG	CGATTTGATT	TTATTGCTA	CTGACGCCCC	TAATTACATT	1200

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2151 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

886

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240

TATGCCTTAA	AGTCGTTGAG	ACAGGCTTAT	TTCTTTTCTC	AAAGCGTGT	TGTAGGGCTT	60
TATCATGGGG	CAAGCATCTT	TGATTTAAAA	TTTGAAGTCT	ATCTTACTAT	GCTAATCTCT	120
TTAATGCCCT	TTGTGGCTAC	GATTTATATC	AATTTCCCAA	AAACCACAGA	AACCTCGCAT	180
GGCTATGCCA	GATGGGCTAA	TGTTAAAGAT	ATAGAATGCT	TTAAAATTTT	TAGCAAAGAG	240
GGCTTTTGT	AAGTGGTGCA	TAGATTAGGG	GTGCAATTG	ATAATGGCTT	TATTCTAGGT	300
AAATTTGGTT	TTCCAAAGCT	TAGAAATGTG	TGCTATGACA	AGCCCTTAGG	AACGATGATT	360
GTTCACCCCC	CTGGTGCTGG	AAAAACTGCA	TGTGTGGCTT	TGCCAAATTT	ATTGACTTTG	420
CCTAATAGCT	GTATTATCAC	TGATATTAAA	GGCGAACTAA	GAGATAAGAC	CGCAGGTTAT	480
AGACAAAAAT	TCCTAAACAA	TAGAATTTTA	ATTTTAAATC	CTTATGGTGA	TGATAACACT	540
TGCTATTTCA	ATCCTTTTGA	TAAAAGGATT	GTTGAAAAGA	TGACCTTTGC	GGAGCAATTA	600
AGGCATGTTA	AAGCAGTAGG	CGATGCTATT	TTGTAGATG	AAGAAGACCA	TTGGGTATCT	660
AAAGCTAAAG	AGCTTTTGT	CTTTTGTGCT	CTTTTACAAG	TAGTAACCAA	AGGGCATAGC	720
TCCTTTTATG	ATGCTCTCTAT	CGCACCAGCT	AATGATTATG	CCCCCTTAAT	ACACCCTAAA	780
AGCCCTTATT	ACAAGCAACT	TTACCAACAC	GATAAAAAGA	CAGGCGAAGT	TATCTTAGAC	840
CCACAACTA	ACGCCCTTAT	GAAAAATCCC	CAAGCTAATG	TTTTAAACT	CTTTTAAAT	900
CAAGTGGCTG	ACCAAAAAATA	CATAGATATG	AATGATGAAA	AAAACTATGA	CCCAAGAGAA	960
CCTGAACCCC	CTTATGGAAC	AAAAGGGGCC	TTAGATGAGA	TTATAAGGAC	AGATGCTAGG	1020
AGTTGGGCAA	ACACTCCTGA	TGATGAATTT	GGGAGCATT	TGTCTTCTTT	TAAGCGTTT	1080
ATGTATGTCT	ATAAAGACCC	AAAAGTGCCT	GAAGCTACTT	CTAAATGAG	CTTTGATTAT	1140
GAAGAATTAA	GAACGGGCAA	TATCAGTATT	TACATTGTAA	TCGCTCAAAT	TGATATAGGC	1200
ACACTTTCTT	CTTTAGTAAG	AGCCTTTCTT	GAGAGTATTG	CTAAAAACCT	TATGGTCAAA	1260
GAAAGCTCTA	ACCTGAAGA	GCGTATTTT	ATCATTGCTG	ATGAATTGT	TAGATTTGGT	1320
AAGTTGCCCT	TCTTGTTAGA	AATGCCAGCA	CTTTGTCGCT	CTTATAATGT	TGTCCCTTA	1380
TTTCATCAGC	AAGATTATGC	TATGATTAGA	AAATACTATA	GCGATGATGA	TTTGAAAATC	1440
TTAAAGGGCG	TGGTGCATTA	TAACATTGTC	TTTAAGATGA	ATAGTGTCTGA	AGATGCTGAG	1500
ATTGTCTCTA	AGGAAGTGGG	CGAATTTACA	AGACGATCTA	AAAATTATTC	TACCGAAAAA	1560
GGTCAATTGG	TCTTTGGAGG	TAGCTCTTCT	TATAGCCATG	AGGGTAGAAA	CTTACTACA	1620
GCCCAAGATA	TTATGAATAT	CAATTTCAGAT	GAAGTCATTG	TTATTGTTAC	AGGGGCTAAA	1680
GCTACCCCCT	TAAAACCTCA	AGCTAATTAT	TGGTTCAAAG	ATAAAGAGCT	TTTAAAAAGA	1740
GCTAATTGTC	CTATTGATTT	AGAAGTAGAG	AGACAAAGAG	TTGAAGAGCC	TATACAACCC	1800
ACTACAGAGA	TTGAAACAAC	CCCTAATCAA	AACAAAGCTG	ACTTAGAACC	AAGTAATAAG	1860
GGGGAAAAAG	TAGAGAAATGA	GAGCAATGAG	AGAAACACTA	ACGAGAATAA	TCCCACTACA	1920
CCACAAGAGC	TTGAAAATTC	AACTTAAAA	GAAAGCGAGA	AAGACAATGA	AAGTCCCATT	1980
ACCTTAGAAA	ATGCTAATGA	AAATATAGAG	CAAGGAAATC	ACAATGAAAT	TGATGAGATT	2040
TTAAAAAGC	CACTGAGTGA	AATCAGTATG	GAAGAGAAAA	GAGCCTTGTT	TAAGAAAAATG	2100
CAACAAAGCG	ATGAAGAAAG	CGAACAAGAA	GTTACACAAA	GCACCCAAAG	T	2151

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...7320
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241

TATAATCATC	CAAAATTTAAG	CGTTGCTGAT	TTAGAATTAG	AGCAACAGAA	TTTAGGAGAA	60
CAAAATGGAA	AAGAGAGAAC	AAATCGCGCA	GATGAGCCGA	ATGGAAC TAG	AGCAGGAATT	120
CCGCAAGAAA	TTACCCGCAG	AAGCGAACCT	AGAGGACAGC	AAGAGGGAAT	GGAGCGATCG	180
AGTGATGAAG	ATCTTTTCACA	CCAAGACCCT	AGTTTATTTA	TTGAGTCTAG	AGAGCAGGGA	240
GGAACAAGAG	GAGTTTATCG	ATCTAGCGAC	CAACAGGCAG	TTTCAGAAGA	ATCCCATAGA	300
GAGCGAGATA	GAATACATGA	ACATGTATCT	AGAGGAGATG	GAGTATCAGC	AAGAGCGGAT	360
GCAAGAGCGA	ATAGCAATGG	AGCATCAAGT	CCAGCAAGCC	GAATGGAAAA	TGGAGCAAGA	420
AGCGAAGAAA	AGGGGGATAA	TCCCAGCGAT	GAGAGAGGAA	TACCACAGAC	ACCGCAATCC	480
CCATCTCATC	AACAAAATAG	CTCCAGAGAT	TTGGGGCTTT	CTCTCTCTAG	AGAACAGCCA	540
GGACAGACTG	GACGCTTACG	CCTTTTGTAT	CATGGACAGA	TGGGCTCATT	ATTTCCCACA	600
GACCATGAAA	ACCAAAGAAA	AAGGAGCGAT	AATGAGCTTG	ATAGACGCAG	TGATAAAGCA	660
AACGAAAATG	GAGACAAAAG	CCCTAGACAG	AATGGAAGCG	CAAATCAAGA	GAGCGCAAGG	720
AGTGAGCGAT	ATGGAATTGC	TCAAGGAAGC	TCAAATCAAT	CAGTATTATT	ACCTGCTCAA	780
AGCCGATTAC	ATCATGCAGG	ACTCAGCGCA	CAAAATGGAC	TTAGAGACCT	TGAAGAAAAC	840
AGGGATCAAG	AGGGAAGACT	TTTATCAAAT	TTAGATAATT	TAGAAAGCTT	GCTTAACGCT	900
ATTAGAAAAC	ACACTATAGC	GAGTGAGCCT	GATTTTAGAT	CCAGGCTCTT	AGAAGCCATT	960
CAAAACAACG	ACTCTTTAAA	AGATAGCATT	GTGGGGGCGC	AACTCCTTAA	AGACCCTAGC	1020
ACTAAAATCT	TTTATGACAA	ATTCCAATTA	AAAATCAGCC	CTAAAAAAGT	CTTAGAGATT	1080
TTAGAAAATC	GCCTTAAAAA	ATCCATTGAA	ACAACGAACG	AAACGCTAAA	CGCATTCAAT	1140
GTGCTGGATG	GTCAGCCCAT	TGATTTAAAC	GCTATCTCTA	ATAGCGTAGG	ATTAAATCCC	1200
ACACAAGAGA	GCAAAATTAAC	AGACAATAGC	GTAGAGTTGA	ATAACGCTCA	AGAACAACC	1260
GCGCAAGAGC	AAACCACACA	AGAACAACC	ACACAAGAAC	AAACCACACA	AGAACAACC	1320
ACACAAGAAC	AAACCACACA	AGAACAACC	ACACAAGAAC	AAACCACACA	AGAGCAAGAC	1380
ACGCAAGAAA	ACGCGCCAAC	CACGATAAAA	CAAGAAACAC	CAATTACGCC	AGCCATCCCC	1440
CTTAATCTTA	AATGAGATT	TAAACCGAGC	GAAGAAGTTT	TAATCAAGGG	AGCTAAAACT	1500
CGCTACAAGG	CTAACATTAA	AGCCATTGAG	CTTTTAAAAG	AATTGCAAGC	CAAAACAAGAG	1560
ATCTTAAAAG	GCGATTACTA	CGCCACTTTA	AAAGAGCAAG	AAATCCTAGC	GCAATTTTAGC	1620
GGATGGGGCG	GTTTAGAGAG	CTACTTTAAA	AAGGCTCAAC	ACCCTGAGGA	ATTTAAAGAA	1680
TTAAACGCCT	TACTCACTAA	AGATGAATTC	AGAAGAGCTT	ATTTGAGCGC	AAGAGACGCT	1740
TACTACACCC	CTAAATTAGT	TATTGATAGC	ATTTATCAAG	GTTTAGATCA	ATTAGGGTTT	1800
AATAACGACA	ACCATCCAAA	AAAAATCTTT	GAACCCAGTT	TAGGCACAGG	CAAATTTATC	1860
GCTCATGCGC	CAAGCGATAA	GAATTACCGC	TTTATCGGCA	CAGAATTAGA	TCCTATTAGC	1920
GCTAATCTTT	CTAAATTCTT	TTACCCTAAT	CAAGTCATCC	AAAACACCGC	TTTAGAAAAAC	1980
TACCAATTCT	ATCAAGAATA	CGATGCGTTT	GTGGGCAATC	CTCCTTATGG	CAATCATAAA	2040
ATCTATAGCT	CCAATGACAA	AGAATTGAGT	AACGAGAGTA	TTCATAATTA	CTTTT TAGGG	2100
AAAGCTATCA	AAGAATTGAA	AGATGATGGC	ATAGGAGCGT	TTGTGGTGAG	TTCTTGGTTT	2160
ATGGATGCTA	AAAACCC TAA	AATGAGAGAA	CACATCGCAA	AAAACGCCAC	CTTTT TAGGC	2220
GCGATAAGAC	TGCCTAATAG	CGTCTTTAAA	GCAACAGGCG	CTGAAGTTAC	GAGCGACATT	2280
GTGTTTTTTA	AAAAAGGCGT	TGAAAAAGCA	ACCAATCAAA	GCTTCACTAA	AGCTATGCCT	2340
TATTATGACA	AGATACTCAA	TAGCTTGGAT	GATGACACCC	TTTTTGCCTT	GCAAAAACAC	2400
CGCTTTTGATA	GTTTTATTCC	TAGCGATCAA	CTTAAGATTG	TCAATGCGGT	TGCAAAACCAT	2460
TTTGGTTTCA	AACAAGAAAA	ATTGCAACGC	TGGTATGAAA	AAATAGACAC	CGCTAACTTT	2520
GGCTACAGCA	CGCAAGATTA	TAAGATCATC	AAAGACTTCA	TTGATAAAGT	TGGAAAGAAAT	2580
AGCATCAATC	TCAACGAACA	AAACCTAAAT	GAATACTTTA	TCCACCACCC	TGAAAACATT	2640
CTAGGGCATT	TGAGTTTGGA	AAAAACCCGC	TATAGATTTG	AAACAAATGG	CGAACAAATT	2700
TACAAATACG	ACTTGCAAGC	CTTAGAAGAT	GAGAGCTTGG	ATTTATCCCA	AGCGCTTAAA	2760
CAAGCGATAG	AAAAATTGCC	TAAAGACGTC	TATCAATACC	ATAAGACTAC	CCTTAAACAA	2820
GACGTTCTTA	TTATTGATTC	AAGTAACGAA	CGCTATCAAG	AAGTTCAAAA	GCTTATCAAA	2880
AATTTAGAAA	GGAGGGAATT	AGTCAAGTGG	GATAATCTTT	ATTTCCAACT	AGAACAAAT	2940
AATGAAATGG	GCATTTTTTT	AAAACCCACT	AAAATCAACT	CTAAAGTCCA	AGATTCACGA	3000
CTAAAAGCCT	ATTTTAAAAAT	TAAAGACGCT	TTGAATGATT	TAACGAGCGC	GGAATTAAAC	3060

CCCTTTAAGCT	CTGATTTAGA	GCTAGAAAAC	AAGAGGGGCTA	AACTCAATCT	TGTTTATGAT	3120
GAATTTGTCA	AGAAATTTGG	CTATCTCAAT	GAGAATAAAA	ATCGTAAGGA	CATCAGACAA	3180
GATTTGTATG	CGCCTAAAGT	CTTAGGATTA	GAAAAAGACT	TTGAAAAAGA	AATAACCCCT	3240
AGAAGCGCTA	AAATGCAAAA	CATAGAACCA	AGGCAAGCTC	AAGCCAAAAA	AGCTCAAATC	3300
TTTTTTGAAA	GGACTTTAAA	CCCTAAAAAA	GAACCTTATTA	TCACTAACGC	TAAAGAGGCA	3360
TTAATTGCAA	GCATCAATCA	AAAAGGGGGT	TTGGACTTGC	ATTTTCATTAG	GGATCATTTT	3420
ACAACCCAAA	GTTTAGAAAC	CACGATTAAA	GAACTTTTAG	AGCAAAAACT	TATCTATAAA	3480
GACCACAAGG	ATAATGGCGG	CTATATTTTA	GCGAACGATT	ATTTGAGCGG	CAACGTGAAA	3540
AGAAAACCTCA	AAGAAGTTAA	AGAAGCCATC	AATCAAGGCG	TGGAGGGATT	AGAGGCTAAT	3600
GTGAAAGATT	TAGAGCTGAT	TATCCCTAAA	GATTTGAAAG	CCACTGAAAT	CATGGCTAAT	3660
ATCAACAGCC	CTTGGATACC	CACTCAGTAT	TTAGAAGAGT	TTTTAATGGA	ATTGAGCGCT	3720
AACCAATTATG	AAAAGCAATA	CGGCGATAAA	ATGACAGATT	ACCAACTAAG	CAATCTCAAA	3780
GAAGACATCA	AAATAGAAC	CCTAAGCGGT	GCTTATGAAG	TTTTTGTTAG	AAACAATGAA	3840
TTAAACGAGC	TTTATGGTAT	CAGGCATAAA	GACAAGCCGC	ATTTCTATAA	AGTGCCTTTT	3900
GAAAGCCTTTT	TAAATAAAGT	CTTAAACAAC	AAGGATTTGA	GCGTTAAATA	CGCCCAAGTT	3960
GATCCTAATG	ACCCTAAAAA	AGAAATATTC	ATCACTGATG	AAGAGCAAAG	CAATCTCGCC	4020
AGACAAAAAG	CAGAAGAATT	GAAAGAAGCT	TTTAAAGACT	GGATTATATA	AGATTATTCA	4080
AGAAGAACCC	ATTTAGAGCA	AATCTATAAT	GACACTTTCA	ACAACCTTGT	TTTAAAAACC	4140
TATGATGGCT	CGCAATTAGA	ACTAGAGGGC	TTTAACTACC	ATATCAGCTT	GCGCCCCCAC	4200
CAAAAGAACG	CTATTTTGTAG	AACCATCCAA	GACAGGGCGG	TGTGTTTAGA	CCATCAGGTT	4260
GGAGCAGGCA	AGACTTTGTG	CGTATAGCC	AGCTGCATGG	AACAAAAACG	CATGGGATTA	4320
GTGAATAAAA	CGCTCATTGC	CGTGCCTAAC	CATTTAACCA	AGCAATGGGG	CGATGAATTT	4380
TATAAGGCTT	ACCCTAACGC	TAATGTGTTA	GTTGTGTATA	GCAAGGACAC	CACTGAAAAA	4440
GAAAGAGAAC	TTTTATTCAA	TCAAATCGCT	AACAACAATT	ATGACGCTGT	GGTTATCGCG	4500
CACACCCATT	TGGAATTATT	GTCTAACCCCT	AGAGGAATCA	TAGAAGAATT	GAAAGAGAA	4560
GAGCTAGTGA	ATGCTGAAAA	AACTTTTGAA	AGGCAAGAAT	TAGCTTATAA	AAATAACCCCT	4620
AGAGAACTA	AAAAACCCAA	TGAAAGAGCC	TTTAAAAACA	AGTTGGATAA	AATCCGTGCT	4680
AAATACGATG	CGATTTTAGA	AAAACAAGGC	TCTCATATTG	ATATTAGTCA	AATGGGGATT	4740
GACAATTTGA	TTGTGGATGA	AGCCCACTTA	TTCAAAAATC	TAGCCTTTGA	AACCTTCTATG	4800
GAAAAAATTG	CAGGACTTGG	TAACCAACAA	GGCTCTAATC	GCGCTAGAGA	TTTGTTTATT	4860
AAAACGCGCT	ACTTGCATCA	AAACGATAAG	AAAATCATGT	TTTTAACCGG	CACGCCTATA	4920
GCTAATTCCT	TGAGTGAAAT	GTATCACTTG	CAACGCTATT	TAACCCCTGA	TGTGTTAAAA	4980
GAAAGAGGGT	TAGAATTCCT	TGATGATTGG	GCTAAGACTT	ATGGGGAAGT	GGTGAATGAT	5040
TTTGAATTAG	ACACTTCCGC	TCAAAGTTAT	AAAATGGTTA	ATCGCTTTTC	TAAATTTAGC	5100
GATGTGCAAG	GCTTAAGCAC	CATGTATAGA	GCTTTTGC	ATATTGTCTC	TAATGATGAT	5160
ATTTTAAAGC	ATAACCCCA	CTTTGTGCGT	AAAGTGTATG	GGGATAAAC	TATCAATGTG	5220
GTGGTGAAGA	GAAGCGAAGA	AGTGGCTCAA	TTCATTGGAG	TGGCTTTAGA	AAATGGAAAA	5280
TATAATGAAG	GCTCTATCAT	TGATAGGATG	CAAAAATGCG	AGGGCAAGAA	AAGCCAAAAA	5340
GGGCAAGACA	ATATCCTTTT	TTGCACCACA	GACGCTAGAA	AAGTGGCTTT	GGATTACCGC	5400
TTGATTGACC	CTAACGCTAA	AGTAGAAAAA	GAATTTTCTA	AAAGCTATGC	TATGGCAAAA	5460
AATATCTATG	AGAATTATTT	AGAACTCAT	GCCACTAAAG	GCACACAAC	TGGTTTCATA	5520
GGGCTATCCA	CACCCAAAAC	CCATAGCCAA	AAAGTCAGTT	TAGAAGCGCT	AGATAACGCT	5580
CACGAACTG	AAAATAAAAA	TCCCCTAGAT	AAAGCTCAAG	AACTTTTAGA	AAGCTTGTCT	5640
AGTTATGATG	AAAAGGGCAA	TCTTATCGCT	CCTAGCAAGA	AAGAATTAGA	GAACGAGCTC	5700
AAAGAGAAAG	AAGCTAAAAG	CGTCAATTTA	GATGAAGAGA	TAGCTAAAGG	CTGTTCTGTT	5760
GATGTTTATA	GCGATGTTTT	AAGGCATTTA	GTCCAAATGG	GTATCCCA	AAATGAAATC	5820
GCTTTTATCC	ATGACGCTAA	AACCGAAGAG	CAAAAGCAGG	ATTTGTTTAA	AAAGCTCAAT	5880
CGTGGCGGAG	TCAGGGTATT	ATTGGGCAGT	CCTGCTAAAA	TGGGCGTAGG	CACTAATGTG	5940
CAAGAAAGAT	TAGTCGCTAT	GCATGAATTA	GATTGCCCAT	GGAGACCTGA	TGAATTGTTG	6000
CAATGGAAG	GGCGTGGGAT	AAGGCAAGGC	AATATTTTAC	ACCAAAATGA	TCCTGAAAC	6060
TTTAGAATGA	AAATCTATCG	TTACGCCACT	GAAAAGACTT	ACGATAGCCG	TATGTGGCAA	6120
ATCATAGAAA	CTAAATCTAA	AGGCATAGAG	CAATTTAGAA	ACGCGCACAA	ATTAGGCTTG	6180
AATGAATTAG	AAGACTTTAA	TATGGGTAGC	TCTAATGCCA	GCGAGATGAA	AGCAGAAGCG	6240
ACAGGCAATC	CCTTGATTAT	TGAAGAAGTC	AAATTGAGAG	CGGAGATTAA	AAGCGAAGAA	6300
TCAAAATACA	AAGCCTTCAA	TAAAGAGCAT	TACTTCAATG	AAGAAAGCTT	AAAAAACAA	6360
GCTTCTAAAT	TGGATTATCT	AAAACAGGAA	TTGAAAGATT	TAGAAACGCT	TCAAAGATCC	6420
GTATAAATCC	CGACTCATAC	AGAGATCAAG	CTCTATGATT	TGAAAAATGA	AGAAAGTAAG	6480
GATTATGAGC	TTATCAAAGT	TAAAGAGGTA	GAGCCTTTAA	AAGAAAACGC	CTCTATGAGT	6540
GAAGAATTAA	CGCACAAGAA	ACTCAAAGAA	CAAAACAAGC	AAATAGCCGA	ACAAAATAAA	6600
GAAAAGCTAG	ACGCTATTAA	AAAGCAATTT	GCAAGCAATT	TGAACACCTT	GTTTGTGAAT	6660
GAAGAAGAAG	ATTATAAGCT	TTTGAATATC	AAGGGCTTTG	TGGTGAATGC	TTATAAAACT	6720
AAGTATCAAG	TGGAGTTTAG	TTTAAAGCCT	AAAGACAATC	CCAATATTGC	CTATAGCCCT	6780
AGCAATATGG	TTTATAAAAA	CGATACTATC	AACATGTTTA	GCTCTTATAA	TTTCTGCGCT	6840
GAGATCAAGT	TTGATGGGTT	TTTAAAAAGG	TTGGATAACG	CTATCACTAA	ACTCCCTGAA	6900
AAAAATCAAG	AATTAGAAAA	CTCCATTGAA	ATCACGAAAA	AAAATATCGC	TAAATACACA	6960

SUBSTITUTE SHEET (RULE 26)

889

AGATTAGTGG	AGCAAAAACC	TTCTTACCCA	CGACTAGAAT	ACCTGCAAGC	TTTAAATGG	7020
GATCATAAAA	CTCTAATAGA	TGATTTAGCT	AAAATGAGCA	AAGACAGAAA	TTATAAGCCT	7080
GCGTTCAACC	CTAAATCTAA	AGAAGTCTTA	AAGAATTGA	ACGCTGAAA	AAGAGCGAGT	7140
TTAGAGAATG	AGAGGGAAGA	GCAAGGGGTT	AAGGGGAACA	CAAAGAGTCA	TGATGAAATA	7200
GAGCCAGCTA	CAGAACAAGT	GATTGAAAAA	GAAATAGAAA	AAGGAGATGA	AATCGCTAAT	7260
AATGTTGATT	ACTACGAGAA	CGAACAAGAA	GTGGAAATTA	CTAAATCAAT	GGGTAGAAGA	7320

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242

AGGGAGGGGG	CGATGAATTT	TTTTGACACC	CTTATGGGTA	TGTTTGTGTA	GCCATCTCAA	60
AAAGTAGCCA	AAAGTCTTGC	TGAACATGTG	GGTAGCTTTT	TTCATGCACA	ACTCATTTTA	120
AACACAATTA	TTACTATTTT	ATTTATGATA	TGGGCGTATA	AGCGTGTGAA	AGAGGGCGAT	180
ATGTTTGAGT	TTAAAACCGC	TATGGGTGTG	GTTGTATTTA	TAGCGTTTGT	AGGATTTATC	240
AATTGGGGGA	TTAAAATATC	TAATGATTTT	AACACTTATT	TTATCAATAC	GATATTCTAC	300
CCATCTGAAA	AAGTAGCCAT	ACTTATCGCT	CAAAGCCTAA	ATGATGGCTT	AGAAATCCCC	360
ACTAACACTA	ATTTAAGTCC	TAGTGAAATT	TTTAGCATAG	GAAATTTAGC	CTCAAGTGCG	420
TATGCAATGA	TAGTTAATCT	GTGGGATAAT	GCTTTTGATG	GTATTAACAT	GTTTAATTGG	480
CTCACAAATG	TACCTAAAT	AATTATGTTT	TTTTTAGTGA	TTTTAGGGGA	ATTATTGTTT	540
TTAGGCTTAT	TGCTTATTAT	TGTGTTATTA	GTTACAGCAG	AAATTTTAT	GTGGTCAGCA	600
TTAGGTTTAA	TTGTATTGCC	TTTAGGTTTA	ATCCCCCAA	CCAAAGGCAT	GTTATTTAGC	660
TATCTTAAAA	AGCTCATTTT	CCTTACTCTT	TATAAACCTT	GTATGATGTT	AGTAGCTTTT	720
TTTAATTATG	GAATAATCTA	TAAAGTCAAT	ACTTTAATCC	CCACTAAACA	CGAAGTCACA	780
CAAGGCTTTT	ATGGCAATGC	GGATAAAATG	GCAAATGAGG	GAAAAATTAT	TGATGTCTTT	840
GGCAATGTCT	TAAAAGGAGA	TGGAACCTCT	TATATAGCCC	ATAGTTCTAT	TGTAGGCTTT	900
TTAACCATTA	TTGTTTTAGG	TTCTGTGATT	TGTTTCTTTC	TAGTCAAACG	AGTGCCTGAT	960
TTTATCAATA	ATATCTTTGG	CACAAGTGGA	GGCGTGGGGG	CAGTAACAGA	AATGATGCAA	1020
AAAATTGGCA	TGACAATAGG	CGGAGCTGTA	TTTGGGGGTA	GTGCAGTTAT	GGTTGCTAAT	1080
CAAGTTAAGC	AAGCCTATCA	GAGTGCTGGG	GGCGGACTAG	CAGGACTTCA	AGCTGGAGCT	1140
AAAGCTTTTG	GGCTTGAGGC	AATCAGTGGA	GGGGCAAGTG	CTATGGCAAA	CCACAGGAGT	1200
GTTAAAGCTG	GGGTGAAACA	CTTTGTAGCA	AGTGTTAAAA	GTGGCTTTGG	ATTTGATAAT	1260
GATAAAAATA	ATAAA					1275

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

890

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1326
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243

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AAGGAGCAAC AAATGGCTTA CAAACCTAAC AAAAGAAGT TAAAGAATT AAGAGAGCAA      60
CCGAATTTAT TTAGCATCTT AGATAAGGCG GATGTTGCAA CAAACAATCC TGTTGAAGAG      120
TCAGACAAGG CCAATAAAAT ACAAGAGCCA CTCCTTATG TCGTGAAAAC GCAAATCAAT      180
AAAGCAAGCA TGATTTCTAG AGATCCTATT GAATGGGCAA AGTATTTAAG CTTTGAAAAA      240
CGAGTCTATA AGGATAATAG TAAAGAAGAT GTCAATTTCT TTGCCAATGG TGAGATAAAA      300
GAAAGTTCTC GTGTTTATGA AGCGAATAAA GAAGGGTTTG AAAGGCGCAT CACTAAAAGA      360
TACGATCTGA TTGATAGAAA TATTGATAGA AATAGAGAAT TTTTATAAAA AGAAATTGAA      420
ATTCTAACCC ACACAAACAG CTTAAAAGAA TTGAAAGAGC AAGGGTTAGA AATCCAATTG      480
ACCCACCATA ATGAAACGCA TAAGAAAGCC TTAGAAAATG GCAATGAAAT CGTTAAAGAA      540
TACGACCATC TTAAAGATAT TTACCAAGAA GTAGAAAGAA CAAAAGATGG TGGATTGGTA      600
AGAGAAATAA TCCCCAGTAT TTCTAGCGCT GAGTATTTCA AGCTTTACAA CAAACTGCCT      660
TTTGAATCAA TAAACAATGA AAATACCAA CTGAATACTA ACGACAATGA AGAAGTTAAA      720
AACTAGAAAT TTGAATTAGC TAAAGAAGTG CATATTTTAA TCCTAGAGCA ACAATTGCTT      780
TCAGCAACAA ATTATTATTC TTGGATAGAT AAAGATGATA ATGCGAATTT TGCTTGGA      840
ATGCATAGGC TTATCAATGA AAATAAACTC AAAGAAAACC ATCTCAGCGC CAATAACGCT      900
AATAAGATTA AGCAATTTTT CTTTAATAAT GGTCTATTT TAGGCTGGAC TAAAGAAGAA      960
CAAAGCGCTA TACAAGAAA CAGAGATTAT TCTTTAAGAA GCGCTCTTTT AAGTTTAGAA      1020
GAAATCGCTC AAGCAAAAAT TGAATTGCAA AAATACTATG AAAGCGTTTA TGTTAATGGT      1080
GATGGGAATA AAAGAGAAAT CAAGCCTTTT AAAGAAATTT TAAGAGACAC CAACAATTTT      1140
GAAAAAGCTT ATAAGGAGCG TTATGACAAA TTGGTAAGCT TGAGTGCAGC AATCATTCAA      1200
GCTAAAGAGG GTGGTAATGA GCGACAAAT TCTAGTGCAA ATAACAATAA CCCTATTAAA      1260
AATACAATAG AGACTAATAC TTCTAACAAT ATTATTCAA ATAATGATAA TATAATCATC      1320
CAAATT

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(2) INFORMATION FOR SEQ ID NO:1244:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244

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ATCAAACATT ACAACAATA TGGCACAGGC TTACATCTAT TTAGGCATAG TTTTGCAACA      60
CTCATTTATC AAGAAACCCA AGACTTAGTT TTAACCTCAA GGGCGTTAGG GCATAGCTCC      120
TACTCTCTA CTAAGATTTA TATTCATACC ACACAAGAGC ATAACAAGAA AGTGGCTCTT      180
GTGTTTGATA GTTTGATAGA GAACAAGAAG

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SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245

AAAAAGAGAA AATACATGCG TTTTAGAAGA GTTAAAAAGC AAAAAAATAA ACACAATAAG	60
GAGCATACAA GTATGGATTT ACAACAAATT GATGAGCTAG AAAAGAAGTT TGAAGAACAA	120
GAAGAACAAG CCCAAGATAC CCCCTAAAA CAAGAGCCTA GCACAAAGGA AGTAAAAATC	180
CCTAAAAAAA GGGGGCGTAA AAAAAGCTTG TTAGATGAAG ATAAGAAAAA GAGCTTTAAC	240
ATTGCCTTTA GTCCTTGTGT GATAAAAGAA CTTAATGAAT TTTTGCTAGA ATTTGGCTCA	300
TTTAAAGAGA CACGAAGCAC TTTTATTGAA GAAGCGCTTA TTAGGCATT AAAACACAGA	360
AAAAACACCC AAGAGCAAAA GCTTTTAAAG CAACTAGAAA GATTACAAAA CAAAGAAAAG	420
GGCAATAATG AAAACAATGA ACTTGAA	447

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246

CTTAATACTG ATAAAATAAC TAAATACTTG ATTATTATTG ATATATTTTT AAAACTTTAT	60
GTTATAATGA TAAGTGAGAT TATTAGTTT CAATTAAAAG GAATAAAAAT GATTAGATTA	120
AAAGGTTTGA ATAAAACTTT AAAACAAGC TTATTAGCTG GGGTTTTACT AGGTGCTACT	180
GCTCCCTTAA TGGCAAAGCC TTTATTAAGC GATGAAGACT TATTGAAACG AGTAAACTA	240
CACAATATCA AAGAAGATAC GCTGACTAGC TGTAATGCTA AGGTGGACGG CTCTCAATAC	300
TTGAATAGTG GTTGGAATTT ATCTAAAGAA TTTCCGCAAG AATATAGAGA AAAGATTTTT	360
GAATGCGTAG AAGAAGAAAA ACATAAACAA GCCCTTAATT TAATCAATAA AGAAGACACT	420

892

AAAGATAAAG	AAGAAGCTG	AAAAAAATC	AAAGAAATTA	AAGAAAAAGC	TAAAGTTT	480
AGGCAAAAAT	TTATGGCTTT	TGAAATGAAA	GAACACTCTA	AAGAATTCCC	AAATAAAAAG	540
CAACTTCAA	CCATGCTTGA	GAACGCTTTT	GATAATGGAG	CTGAAAGTTT	TATTGATGAT	600
TGGCACGAAC	GCTTTGGGGG	TATAAGTAGA	GAGAATACTT	ATAAAGCACT	TGGCATTAAA	660
GAATATAGTG	ATGAAGGAAA	GATATTAGCC	TTTGGCGAAA	GAAGTTATAT	TAGACAATAT	720
AAAAAAGATT	TGAAGAAAG	CACCTTATGAT	ACTAGACAAA	CCTTATCTGC	TATGGCTAAT	780
ATGAGTGGCG	AAAACGATTA	TAAAATTACT	TGGTTAAAAC	CCAAATATCA	GCTCCATAGT	840
TCAAATAATA	TTAAACCCCT	AATGTCAAAC	ACAGAGTTGT	TAAATATGAT	AGAGCTAACC	900
AATATCAAAA	AAGAATATGT	TATGGGCTGT	AATATGGAAA	TAGATGGTTC	TAAATATCCC	960
ATTCATAAAG	ATTGGGGATT	TTTTGGTAAG	GCAAAAGTCC	CAGAACTTG	GAGAAATAAG	1020
ATTTGGGAAT	GTATTAAGAA	TAAAGTAAAG	TCCTATGACA	ACACTACCGC	TGAAATAGGA	1080
ATAGTTTGA	AAAAAATAC	TTATTCTATC	TCTCATCAC			1119

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247

AAAGATTACA	AAACAAAGAA	AAGGGCAATA	ATGAAAACAA	TGAAGTTGAA	TGAATTTTTT	60
ACGCATAAGA	TAATCTATAA	AGACACCCCT	TTAAAGTTTA	AGGATACACT	AGAACAAGAA	120
ATCAGCCAAG	CTAGTTTAGT	AGAGAAGTTA	ATCTTAGCTA	ATATCTTAGC	CAATATGGTG	180
TTTGCTAAGA	TAAGCAATGA	GAATGCCCCCT	AAAATTCTTA	TTTCACGCTT	GATGTGTAAG	240
TTTAGTCCTA	TTGATTATGA	AAGCACTATT	CCTAGTGATT	TTAAGCCTAT	AGATGAAGAA	300
GAATATGAAG	ATGATTTAGA	ATGGCTAAAT	GAAGAAAAAG	AAGATAGGCT	CTTTAATTAC	360
TATCTATTTT	TAAATGGTAT	TAAAGAAAGT	GATGTAGAAG	AAGTGTTTAA	TGAAAGTGTA	420
GAAATCTATG	ATGAGTGCTT	AATAGAAATC	GCTCAAAATG	TCCTTAAAGA	TAAATTTTCT	480
TATGACATTG	ACTTATTGCA	AGTTTTAGTA	AAAGGTTATG	CTAAAGAGAT	TAGAGAATTT	540
TTGAGTTATA	AACCTATAAA	AGAAATCAAA	GACTTTAAAG	ACAAAGACAC	CGCACTTTAT	600
ATCAGCTTAG	GAAAAGACTA	TGACAAAGAA	AAAGAGCCAT	TTTCTAAAAA	ATTGCAACAA	660
TGTTTTAAAG	AGATTTTAGA	GAGCAAGGGT	ATT			693

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

893

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248

ATGAAAGGTT	TAACAATGAA	AAAATTAGTT	TTTAGCATGC	TTTTATGTTG	TAAAAGCGTG	60
TTTGCAGAGG	GGGAAACTCC	TTTGATTGTC	AATGACCCAG	AAACCCATGT	AAGTCAAGCC	120
ACTATCATAG	GCAAAATGGT	AGATAGTATC	AAAAGATACG	AAGAGATTAT	TTCTAAGGCT	180
CAAGCTCAAG	TCAATCAGTT	ACAAAAAGTC	AATAACATGA	TAAATACGAC	TAATTCTTTG	240
ATTAGTAGTA	GTGCTATCAC	TTTAGCCAAT	CCTATGCAAG	TTTTACAAA	CGCTCAGTAT	300
CAAATAGAGA	GCATTAGATA	CAACTATGAG	AATTTAAAGC	AAAGCATAGA	AAATTGGAAC	360
GCACAAAATT	TGTTAAGAAA	CAAATACTTA	CAGCAACAAT	GCCCTTGGCT	TAATGTCAAT	420
GCTCTTACTA	ACAATAAGAT	TGTCAATCTT	AAAGATCTCA	ATAACCTAAT	CACCAAAAAT	480
GGCGAACAAA	CCCAAACCGC	AAGAGATGTG	CAAAATCTCA	TTCAGTCCAT	TAGTGGCAGT	540
GGCTATGGAA	ACATGCAATC	ACTTGCTGGG	GAATTGAGTG	GTAGAGCGTG	GGGGGAAATG	600
TTGTGTAAAA	TGGTAAACGA	TAGTAATTAT	GAAAGCGAGC	AAGCTCTTTT	AGCAACAGGC	660
AATAACCCAG	AAGAGCAAAA	ACGAAGATT	TTGCTTAGAG	TAAAGAAAA	GGTTAATGAT	720
AATAAGCAGT	TAAAAGATAA	ACTTGACCCA	TTTCTAAAA	GACTTGATGT	CCTACAAACT	780
GAGTTTGGTG	TAAGTACCC	TACAGCTAAC	CATAATAAGC	AAGGGATACA	TTATTGCACA	840
GAAATAAAG	AGACAGGTAA	ATGCGACCCT	ATTAAAAATG	TATTTAGGAC	AACTCGCTTA	900
GATAACGAAT	TAGAACAAGA	AATCCAAACG	CTCACACTTG	ATTTAACCAG	AGCCTCCAAT	960
AAAGACGCTC	AAAGCCAAGC	CTACGCAAT	TTCAATCAAA	GGATTAAATT	ACTTACTCTA	1020
AAATATTTAA	AAGAAATTAC	CAATCAAATG	CTCTTTTAA	ATCAAACAAT	GGCAATGCAA	1080
AGCGAGATTA	TGACAGATGA	TTATTTTAGG	CAAAATAATG	ATGGCTTTGG	GGAAAAAGAA	1140
AACCATATAG	ACAACAATT	AACGCAAAAA	AGAATAACG	AAAGAGAAAG	AGCTAGAATA	1200
TACTTTCAAA	ACCCTAATGT	TAAATTTGAC	CAATTTGGCT	TTCCCATTTT	TAGTATATGG	1260
GAT						1263

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1338 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249

AAGCGTTGCT	GGTATTTCTG	GCGAGCGTTT	TTAAACAGGA	GTTTTGCTCC	CTTACTCAAC	60
CCTAACGAGA	ACCTTTTAGA	TCAAGTTAAG	TCTAGCATT	TTTTAAAAA	AGGGGTGTCT	120
TATTTTGACT	GGGGGGCTTC	AGGTTTGCG	AGTGCTTTAG	TGGAAAAGCG	CGTGAAATCC	180
TTACTGCCTT	ATTATGCGAA	CGCTCATTCT	GTGCTTCTA	AACATGCGAT	TTTAATGGGC	240
ATGCTTTTAA	AAGAATGCCA	AGAAAAGTTA	AAGCGTTCTT	TAAATTTGAG	TGCTAATCAT	300
TGCGTCTTGA	GCGCGGGGTA	TGGGGCGAGT	TCAGCGATTA	AGAAATTTCA	AGAAATTTTA	360
GGGGTGTGTA	TCCCTTCAAA	AACGAAGAAA	AATTTAGAGC	CGTATTTGAA	AGATATGGCT	420
TTAAAGCGTG	TGATTGTAGG	GCCTTATGAG	CATCATTCTA	ATGAAGTTAG	CTGGCGTGAA	480
GGCTTGTGTG	AAGTGTGCG	TATCCCTTAA	AATGAACATG	GTTTATTGGA	TTTAGAAATT	540

SUBSTITUTE SHEET (RULE 26)

894

TTAGAGCAAA	CTTTAAAAAA	AACCCCTAAC	AGCTTGGTTT	CTGTGAGCGC	GGCTTCTAAT	600
GTAACGGGAA	TTCTTACGCC	TTTAAAGAA	GTTCATCAT	TGTGTAAGGA	ATATAGGGCT	660
ATTTTAGCTT	TGGATTAGC	GAATTTTAGC	GCGCATGCTA	ACCCTAAAGA	TTGCCAATAC	720
CAAACCGGTT	TTTATGCGCC	TCATAAGCTT	TTAGGGGGCG	TTGGAGGGTG	CGGTCITTTA	780
GGCATTCTTA	AAGATTGAT	TGACACGCAA	ATCCCTCCGA	GTITTAGCGC	AGGGGGCGTG	840
ATTAAATACG	CTAATCGCAC	ACGGCATGAA	TTTATTGATG	AATTGCCTTT	AAGAGAAGAA	900
TTTGGCACGC	CAGGATTGTT	GCAATTTTAC	AGGAGCGCTC	TAGCGTATCA	ATTAAGAGAT	960
GAATGCGGTT	TGGATTTTAT	CCATAAGAAA	GAAACAACC	TTTTAAGGGT	GCTTGTGTAT	1020
GGCTTAAAAG	ACTTGCCCGC	TATTAATATT	TATGGGAATT	TAACGGCGAG	TCGTGTGGGG	1080
GTAGTGGCTT	TTAATATTGG	AGGGATTTCG	CCCTATGATT	TAGCGAGGGT	TTTAAGCTAT	1140
GAATACGCTA	TTGAGACCCG	GGCGGGTTGC	TCTTGC GCGG	GGCCTTATGG	GCATGATTGG	1200
TTGAATCTTA	ACGCTCAAAA	GTCAAGCGAT	TTTAACGCTA	AACCCGGATG	GCTTAGAGTG	1260
AGTTTGCAC	TCACGCATTC	CATAACGAT	ATTGATTATT	TGCTAGACAG	CTTGAAAAAA	1320
GCGGTGAAAA	AATTGCGT					1338

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250

TATGTGATAG	AGCTTGACAT	TAACGCCAGC	GATAAATCGC	TCTCGCACAG	AGCCGTTATT	60
TTTAGCCTGC	TCGCTCAAAA	ACCTTGTTTC	GTGCGGAATT	TTTTAATGGG	AGAAGATTGT	120
TTAAGCTCTT	TAGAAATCGC	TCAAAATTTA	GGGGCTAAAG	TGGAAAATAC	CGCCAAAAAT	180
TCTTTTAAAA	TCACACCCCC	AACAACATATA	AAAGAGCCTA	ATAAGATTTT	AAATTGCAAC	240
AATTCTGGCA	CTAGCATGCG	TTTATACAGC	GGGCTTTTAA	GCGCTCAAAA	AGGCCTTTTT	300
GTTTTAAAGCG	GGGACAATTC	CCTAAACGCA	CGCCCCATGA	AAAGAATCAT	TGAGCCTTTA	360
AAGGCGTTTG	GGGCAAAGAT	TTTAGGGAGA	GAGGATAACC	ATTTTGCCCC	CTTAGCGATT	420
GTAGGGGGTC	CTTTAAAAGC	TTGCGATTAT	GAAAGCCCTA	TCGCTTCAGC	TCAAGTCAAA	480
AGCGCTTTTA	TTTTAAGCGC	CTTACAAGCT	CAAGGCATAA	GCGCCTATAA	AGAAAGCGAG	540
CTTAGCCGTA	ACCACACAGA	AATCATGCTT	AAAAGTTTGG	GGGCTAACAT	TCAAAATCAA	600
GACGGCGTTT	TAAAAATTTT	ACCCCTAGAA	AAACCCCTAG	AATCCTTTGA	CTTTACCATA	660
GCCAATGATC	CGTCTAGCGC	GTITTTTTTA	GCTCTCGCTT	GCGCGATTAC	GCCAAAAAGC	720
CGCCTTCTTT	TAAAAAATGT	CTTGCTCAAC	CCCACTCGCA	TAGAAGCTTT	TGAGGTTTTG	780
AAAAAAATGG	GCGCTCATAT	AGAATATGTT	ATCCAATCCA	AAGATTTAGA	AGTTATTGGC	840
GATATTTACA	TAGAGCATGC	CCCTTTAAAA	GCGATCAGTA	TTGATCAGAA	TATCGCCAGC	900
CTTATTGATG	AAATCCCCGC	TTTAAGCATC	GCTATGCTTT	TTGCAAAAGG	CAAAAGCATG	960
GTGAGAAACG	CTAAAGATTT	ACGAGCCAAA	GAAAGCGATA	GGATTAAAGC	GGTTGTTTCT	1020
AAATTCAAAG	CTTTAGGGAT	TGAGTGCGAA	GAATTTGAAG	ACGGGTTTTA	TATAGAGGGA	1080
TTAGGAGATG	CGAGTCAATT	AAAGCAGCAT	TTTTCTAAGA	TTAAACCCCC	TATTATCAAG	1140
AGTTTCAATG	ATCACAGGAT	TGCGATGAGT	TTGCTGTTT	TAACTTTAGC	GTTGCCTTTA	1200
GAAATTGATA	ATTTAGAATG	CGCGAACATT	TCTTTCCCAA	CTTTTCAGCT	TTGGCTCAAT	1260
CTATTCAAAA	AAAGGAGTCT	CAATGGAAAT				1290

(2) INFORMATION FOR SEQ ID NO:1251:

SUBSTITUTE SHEET (RULE 26)

895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251

AATGCGCGAA	CATTTCTTTC	CCAACCTTTC	AGCTTTGGCT	CAATCTATTC	AAAAAAGGA	60
GTCTCAATGG	AAATTAAAT	GGCTAAGGAT	TATGGTTTTT	GTTTTGGCGT	CAAAAGAGCG	120
ATACAAATCG	CTGAAAAAA	TCAAAACAGC	TTGATTTTTG	GCTCGCTCAT	TCATAACGCT	180
AAAGAAATCA	ATCGTTTGA	AAAAAATTTC	AATGTGAAAA	TTGAAGAAGA	TCCTAAAAAA	240
ATCCCTAAAA	ATAAGAGCGT	GATCATAAGA	ACCCATGGCA	TTCTTAAACA	GGATTTAGAA	300
TACTTGAAAA	ATAAGGGGGT	TAAAATCACT	GACGCGACTT	GCCCGTATGT	GATCAAACCT	360
CAGCAAATTG	TGGAATCCAT	GAGTAAAGAA	GGGTATCAAA	TCGTGCTTTT	TGGGGACATT	420
AACCAACCTG	AAGTCAAGGG	CGTGATCAGC	TATGCCACTA	ACCAGGCTTT	AGTCGTCAAT	480
TCGTTAGAAG	AATTGCAAGA	AAAAAATTG	CAACGGAAAG	TGGCTTTAGT	CTCTCAAACC	540
ACCAAGCAAA	CCCCAAAAC	CTTGCAAATC	GCTTCT			576

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252

AAATTACCAA	TCCACGCATT	CGTTTTAATG	TGTTTAGCGA	TCCCTCTAA	AGTCATAGCC	60
ATTAACGATA	ATGTGGCACT	CTTAGAGACT	TGGGCGTTTC	AAAGAGAAGC	GAGCTTGGAT	120
TTAATGGGCG	AGTCCGTAA	AGTGGGCGAT	TATGTGCTAC	TACACATCGG	CTATGTGATG	180
AGTAAGATTG	ATGAAAAAGA	AGCCCTAGAA	TCCATTGAGC	TTTACCAAGA	AATGATCGCC	240
GAAGTGAACG	AAACGCATGA	A				261

(2) INFORMATION FOR SEQ ID NO:1253:

SUBSTITUTE SHEET (RULE 26)

896

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...738
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253

AAAGGAACAA	GCATGAGCGA	ACAACGAAAA	GAATCGTTAC	AAAATAACCC	TAATTTGAGT	60
AAAAAAGACA	TCAAAATCGT	GGAAAAGATT	TTGAGCAAGA	ACGACATTAA	AGCCGCTGAA	120
ATGAAAGAGC	GCTACCTTAA	AGAAGGGTCT	GTATGTGTGA	ATTTTCATGAG	TTCTCCCGGT	180
AGCGGTAAAA	CCACGATGTT	AGAAAATCTA	GCGGATTTTA	AAGACTTTAA	GTTTTGCGTG	240
GTAGAGGGCG	ATTTGCAAAC	CAACAGGGAT	GCGGACAGGT	TGCGTAAAAA	AGGCGTGAGC	300
GCGCATCAGA	TCACCACCGG	CGAAGCGTGC	CATTTGGAAG	CGAGCATGAT	TGAGGGGGCG	360
TTTGATTTAT	TAAAGATGA	GGGAGCGTTA	GAAAAAAGCG	ATTTTTTAAT	CATTGAAAAC	420
GTGGGGAATC	TGGTTTGCCC	CTCAAGCTAT	AATCTAGGGG	CGGCGATGAA	TATCGTTTAA	480
CTCTCTGTCC	CAGAGGGCGA	TGATAAGGTG	CTAAAATACC	CTACGATGTT	CATGTGTGCG	540
GATGCGGTCA	TTATCAGTAA	GGCGGACATG	ATTGAAGTGT	TTAATTTTAG	GGTTTCTCAA	600
GTCAAAGAAG	ACATGCAAAA	ATTAAAGCCT	GAAGCGCCCA	TTTTTTTAAT	GAGCTCCAAA	660
GACCTAAAAA	GCTTGAAGA	TTTTAAAAAT	TTCTTTTAG	AAAAAAAGCG	TGAAAATAC	720
CAATCCACGC	ATTCGTTT					738

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2871 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2871
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254

GGAAAAATAA	TGGCAAAGAA	AAAACAAGAA	GTAAGGAATA	ATGAAATTTT	TGTCGCTCAA	60
AAACTCGCTG	AAGAGGAATT	GAACGCTAAC	GAGATTAACG	ATCCGTTAGA	AATGCTGGAC	120
TTTAAAAGCT	TTGATGATAA	TAAGGAGCTT	TTAGATTACC	AACAGCAAGC	TTTGATTAA	180
GCTTTTAGAG	TGCTTGTTGC	TTATTTTAGA	GACTTCAAAG	AAAGTAAAAA	AGAATTTTAC	240
GCTTTTTATC	AAAAGCATT	TTTATTCGCT	AATTGCGATT	TCGCTAAAAA	GAAACTCAAT	300
CATTGTGTTA	AGAGCCATT	TAAGGTAGAA	AATCATTGCG	TGCGTTTTGA	AAATTTTCATC	360

SUBSTITUTE SHEET (RULE 26)

AACCGCCTAG	CCTTTTACAT	GGCCACAGGG	AGCGGTAAAA	CGATCGTCAT	TATCAAACCTG	420
GTAGAGCTTT	TAAGCGTGGC	TATGGGAATG	GGTTTGATCC	CTAAGAAAAA	TATCATGTTT	480
TTTAGCGCGA	ACGAGCATT	AATCAAGCAA	TTTGAAAAAG	AAATTGAAAA	ATACAACCGC	540
AATAAGGACT	ATTCCAAACA	AATTGATTTT	AAAAACCTTA	AAAGCGTTAA	GAATAAGGAT	600
TTTATATCGTG	CTCCAAAAGA	TTCTTTAATG	AAAGAAATCG	CTCTTTTTTA	TTACCGCGCA	660
GATTTAATGA	GCGATGAAGA	AAGCAAGGAA	AACCTTTTAA	ATTATAAGGA	TTGTTGGGAT	720
AATGGGGAAA	ATTATGTGAT	TTTAGATGAA	GCGCATAAGG	GGAATAAGAC	TGAAAGCAAA	780
AGACAGGCGA	TTTTTAGCCT	GCTGTCTTTA	AAAGGGTTTT	TATTCAATTT	CAGCGCCACT	840
TTCACTGAAG	AAAGCGATCT	CATCACTGCG	GTGTATAATT	TGAGCGTGGG	CGAGTGGGTG	900
AAACTTGGCT	ATGTTAAAGA	GTCTGTTTTA	TTGAAGAAAA	ACAACCTTAA	CGCTTTTAAG	960
GAATTGAAAG	ATTTAAACGA	CAGGGA AAAA	GAAATCGCTC	TTTTAAAGGC	GTTATTGCTT	1020
TTAGGCATGC	AAAAACGCTA	TAAAGTAGAA	GGCTATTTTC	ATGACCCTTT	AATGCTCGTG	1080
TTACGCATT	CTGTGAACAT	GGAAAACAGC	GATGCGGAAA	TCTTTTTTAA	AACTTTAGCG	1140
CGCGTGATTG	AAAATGATGA	TGAGAGCGAT	TTTTCAAAAG	CTAAAGACGA	TTTATTAGAG	1200
GAATTAAAGA	ATCCGGAATT	CCTTTTTAGC	GATGGCAAAG	ATAAAGAAAA	AGACTATAAA	1260
ATTGAGGTCT	TTAAAGAGAG	TTTAAAGGGC	ATGGATTTTA	AAGGCTTAAA	AGAAGCAGTT	1320
TTTTATGCCA	GTAATGGGCA	TATTGAAGTC	ATCATTAAAC	CTAAAAACAA	CCAGAAATC	1380
GCTTTCAAGC	TCAACACGAG	CGATAAAGTC	TTTTGCCTGA	TTAGAATAGG	CGATATTACA	1440
GAATGGATCC	GTGAAAAATT	AAAGAGCGTG	AAGGTGGTGA	GTAAGAAATT	GAGCTTCAAA	1500
GAAGAGAGCT	ATTTAGCCA	GATTGATAAG	AGCAGTATCA	ATATCTTAGT	GGGGTCTCGT	1560
GCTTTTGACA	CTGGGTGGGA	TAGCACAAGG	CCTAGCGTGA	TTTTATTTTT	AAATATAGGG	1620
CTTGATGATG	ACGCTAAAAA	GCTGGTGAAG	CAATCTTTTG	GCAGGGGCGT	AAGGATTGAA	1680
AGCGTCAAAA	ACCAACGCCA	AAGGTTAGCG	TATTTAGAGA	TAGATGAAGC	CATTAAAGAC	1740
AAGCTGAAAC	CAAACGCTGC	AATGCTGGAA	ATGCTTTTTG	TGATACCTAC	CAACCATGCA	1800
AGCCTTGAAG	CGATTTTAAA	GTTCCAAAAA	GAGAGCGAAA	ATGGGGGTGA	GAATAGAGGT	1860
CCTTGGCGTG	AAATCAAATT	AGAAAAAACG	CGCATAGAGC	ATGCCTTATT	CGTGCCTTGC	1920
TACCGAAAAG	AACAAACCAA	CGCTCTTAAA	ATTTCTCAAA	GCGCTTCGTT	TAAAATGAGC	1980
GAAAAAAATT	TTAAGGATTT	AAAAGAGCAT	TTTCATTTAA	TGAGTGAAAA	GCATTTTATT	2040
TTAAAGCATG	AAATTTATGA	CCCTAAAGAT	TACGCGCTGT	TAAAAGAAAT	GATACAAACA	2100
GCGCATTTTA	AAAAGGTATC	AACCTGGCAT	TATAAAGATT	TAGATTACAT	GATTTCTGAA	2160
ATTAAAGGCA	AGCTATACCC	TAATCAAAAA	GTGCCTAAAG	ACGAGTTTAA	CGCCCTAGAT	2220
AATGAGAAAA	TCGTGCATTT	TAAAAGGGTT	AAAGTTAAGG	CGGATAAAAA	AGAAAAATTG	2280
ATTCAAACCA	TCCAAGAAGT	GAAAGAGCAT	GCGCCTTTGG	ATAAAGAAAC	TTTAAGAAAA	2340
AAAATCGCGC	AAGGCGAGAT	CGATCCTTAT	GATACAGAAA	AACACAAACA	AGACAGAACG	2400
TTCAAAGTTG	GTGATGCAGA	GCTGTTAAAA	CTCAAAGAGC	ATTACTACAC	CCCCCTCATT	2460
AAAGCCAAAA	ACTGCGATTG	GCTTAAGCAT	GTGGTTAAGG	TAAAGAGCGA	GAGCGATTTT	2520
TTAGAAGAGT	TGTTAAAGAT	TACCGAAACG	CTGCAAGAAA	ACTATGATTT	TTGGGCGTTC	2580
AGCAAGATTG	ATGAGCATTT	AGACAATTTG	TTTATTCCTT	ATATAGACAA	CGCTACAGAA	2640
AGGCGCTTTT	TCCCTGATTT	TATCTTTTGG	CTGCAAAAAG	GCGGCACGCA	GATCATTTGC	2700
TTCATTGATC	CTAAAGGGAG	CAAACACACT	GATTACGAGC	ATAAGGCAGA	TGCGTATCAA	2760
CTTTTGAAG	ATAAGGTTTT	TAACCCTAAA	GACGATCCCA	ATCTCAAAAT	CAAAGTGTTT	2820
TTAAATTTT	ATGGGGATAA	GGATGATGTG	GGGGAGCGTT	ATAGGGATCT	T	2871

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...747

SUBSTITUTE SHEET (RULE 26)

898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255

TGCATGCGTT	TTTATTTTAA	ATTCTTTTGG	CTTTTAGGGA	TTTTTCTTAT	TTTTTATTTT	60
TTAGACATTA	AAGGCAGCTC	TTCTTATATC	AGCGACCGGG	TTAAAAGCGC	CTTGATGAGC	120
GCGAAAAACA	GCTTACTAGA	CAACGTTCAA	GCGTATTTTT	TTCAAGCCCA	AAACATTAAAG	180
GAATTTCAAA	AAGAACGCTT	GATTTTAGAA	GCTTTAAAAC	TAGAAAACGC	TGATTTGAAA	240
GAGCGTTTGA	ATAGTATTTA	TCCTTTAGAA	AATCCAAAAA	TGACTTATAC	CCCTACTTTC	300
ATGACTTCAT	TCATCAATTT	AGAAGACACA	CACAGCGTTT	CTCTCAACCC	TATTGTGAAT	360
TTAGAAGAAA	ACAAGATTTA	TGGCCTTGTC	TCTCACAACC	AAGCCATAGG	CATTGCCGTG	420
CTAGAAAAAG	GGCGCTTGAA	CGGGTTTTTG	AACGCCCACA	AGCGGTGTGC	TTATAGCGTG	480
ATGATAGGCC	AAAATCAAGT	CTTAGGCTTT	ATAGGGACTA	ATTTCAAGCA	AGAATTAGTC	540
GTGGATTTC	TTGTCCCAAG	CGCTGAAATC	AACATAGGCG	ATCAAGTGCT	AACGAGCGGG	600
CTAGATGGGA	TTTTTGAGC	GGGGGTGTTT	GTGGGTGAAG	TTTCAAGCGT	TGAAGATCAT	660
TACACTTATA	AAAGCGCGGT	GTTGAAAAAC	GCTTTTTTAA	GCGAAGCCAA	ACTTTTAAGG	720
CATGTGTTTT	TAAGCGGTGT	GAAAAAC				747

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256

TGGTATTTTA	AAAAAGAAAG	AAATCCCATG	GTTATACATG	AAAAAATCAA	AAGCCGCTTT	60
TCTAGGAATT	GGTCTTTAAG	GAATAGGGGC	AGGCATTTTG	CATCTTCAAG	CGTGTATTTT	120
TTCTCACTTC	TTGTCATTAC	AGCGGTTAAT	AGAAGTAGTG	CAGTTGCTTG	GTTATTGATG	180
CCTGAACATT	TGATTGGGTG	GTTTTTGATT	TCTTTTAGTG	GGGAATTTGT	AGCAGACATG	240
GCGTTTGGCA	AAAAAAGTAA	GATTTTTTAA	ACCCGCTTTG	GAATTTCTAT	TGTGAGCGGC	300
GTTTCACTAT	TGCTTGCGC	TTTACCAGCG	CATTTATTTT	TTGTATGGTT	TGGCTTTATT	360
AATTGGTGGG	CTGTCTTTTT	TATAGAAGCG	GGAGCTGATC	TATTGGTGGG	CTGTGTGATA	420
CAAAAGATTT	TTTTTGGTAA	ATATTGGGTG	GATCGCTATT	AT		462

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

899

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257

TGGGCGAAAG GCGCTGGGGC TTTAGTGCTT GAAGAATACG AGAGCGCGAA AAAAAGAGGG	60
GCTAAAAATT ATGCAGAAAT TGCCGGGTAT GCGAGAGCG GCGATGCTAA CCACATCACA	120
GCCCCAGCCC CTGAGGGTGA AAGGGCTTTT AAAGCCATGA AAATGGCTTT AGAAATGGCG	180
AAAGTGAAG TATGCTATGT GAACGCCAT GGGGACAAGC ACGCATTA	228

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258

ACGCCCATGG GGACAAGCAC GCATTATAAC GATTGGTATG AAAGCATTGC GTTAAAAAAT	60
GTGTTTGGCT CTAAGAAAA AGTCCCTCCT GTTAGCTCCA CTAAAGGGCA GATTGGGCAT	120
TGCTTGGGTG CTGCGGGCGC GTTAGTAGCC GTTATTTCTA TCATGGCCAT GAATCAAGGG	180
ATCTTACCTC CTACCATTAA TCAAGAAACG CCTGACCCAG AATGCGATCT GGATTATATC	240
CCTAATACAG CCAGAGAAAA GCAAGTGAAT GCGGTGATGA GTAACCTATT TGGTTTGGT	300
GGCACTAATG GTGTTGTGAT TTTCAAAAAA GCC	333

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...567

SUBSTITUTE SHEET (RULE 26)

900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259

GGCCCAATAC	AAAGCGCTCC	AGCAATGAAC	AAGCTTTTTT	TAGCTTTTAT	TGTTGGGGGA	60
ATGCTTTTAA	GTGCTGATGC	TTTAAACGAT	AAGATTGAGA	ATTTAATGGG	GGAGCGATCC	120
TACCACATGA	ACAAGCTTTT	TTTAGAGCGT	TTGTTTAAAA	ATCGTAAGGA	TTTCTATGAA	180
ATGGGGCGTT	TGGATTCCCT	AAAACACTC	AACACTCTCA	AAGAAAACGG	GCTTTTATCG	240
TTTAATTTTG	ACAAACCAAG	CGTGTTAAAA	ATCACTTTCA	AGGCTTCAAG	TAATCCCCTA	300
GCGTTTGCCA	AAAGCATCAA	CAATTCTTTG	AATATGATGG	GGTATTCGTA	TGTTTTCGCT	360
ATTAGAATGC	AAAGCTCTTC	AGGCGAGAAT	GTTTTTTCAT	ACGAGCTTAA	AACGGAATAC	420
GTTTTAGACC	CTAACATTTT	GATAGAGACG	ATGAAAAGGC	ATGGTTTTGA	TTTTATGGAT	480
ATTAGACGGG	TGTCTTTAAA	GGAGTGGGAA	TACGACTTTG	CCTTACAAAA	GATCAAGCTC	540
CCTAACGGCG	AGAGCCTTAG	TTTTGAG				567

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260

ATGGAACAGA	ATAAAAAAAG	TTTAGAAAAT	TTAGATCTTT	CTGATGTTCA	AAACATTTCT	60
AAAGATATTT	CTGGAACGGC	TTTAGAAGAA	TTATCGCTTA	AAAATTTAGA	TAAAAATTTG	120
CAGATTCTAA	AAGAAGTTGG	AGCGGCAGAA	ATTTGCAAGG	CGACTAAAAT	CGCTTCTAAA	180
AATATCCATT	CTATCTTGGA	AAAGCGCTAT	GAGTCTTTAT	CAAGGGTGCA	TGCTAGGGGT	240
TTTATACAGA	TTTTAGAGCA	CGAGTATAAA	ATTGATTTGA	GCGCATGGGT	GAAAGAATTT	300
GACAAAGTGT	GTGTTTTTAA	AGAGGGCGTG	GGAGAAGAGC	AAAAACAAGA	AACAAGCCCCT	360
GAAGAAACAG	CAAAAAAACC	CCTTAAGGTT	GAATTGGATT	ACAGCATCAA	TCAAGCCAAT	420
ACTTCATTAT	CCAAAAATC	TTCCAAATGG	AAACCCCTTG	TTATCGTTTT	AGGGGTGGTT	480
GTCATTATTT	TAGTGGTCGT	TATCATTCAA	AACAGCTCTT	CTTTAAAAGA	AGAGAGAGAG	540
CAAGAACGCG	CTATTAGGCC	CGACACCAAA	AATAATCTTT	TCAATGAAAC	TAATCCTACA	600
GAAGAAAAAA	AGTTAGAGCC	AACGCCTAAA	TTAGAAGAAA	AACACAAAGA	ACAAGACAAG	660
CAAGGCAAAG	AAGCGATCAA	AGAAAATCCT	AATACCATTT	ACATTATCCC	TAAACGAGAT	720
ATTTGGGTAG	AAGTGATTGA	TTTAGATGAG	AAAAAAAAC	CTTTTCAAAA	GGTTTTTAAA	780
AAAAGTTATC	CTTTAGAGGC	TAAAACCAC	CGCTTGTTGT	TACGCTTTGG	GCATGGGCAT	840
CTTATTCTTA	AAAACAACCA	TCAAGAACAA	GATTATAACG	ACAGCAAAAC	TAGGCGGTTT	900
TTATACGAGC	CAATAAAGG	TTAACGCTC	ATCAATGAGG	CCCAATACAA	AGCGCTCCAG	960
CAA						963

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

901

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261

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AGGAGTGGGA ATACGACTTT GCCTTACAAA AGATCAAGCT CCCTAACGGC GAGAGCCTTA      60
GTTTTGAGTA GCGATCCTGT GGAGTTTAAG GAAGCGAGCG GGAAATATTG GCTGAGCGTG      120
AATCAAAACG CGTATTTAAA AATAAGCTCC AATAACCCCTT TGTGGCAACC CAAAATCATT      180
TTTTATGATG AAAACTTAAA GATCATTCAA ATCATTGCTA AAGAAAACAG ACAACAAGAA      240
ATCGCTCTTA ACTTGCTTGA TGGCGTGGCT TTTATCCATA TCACTGACGC AAAAAACCCT      300
ATCATTTTAA AAAATGGGAT TAGCGTGGTT TTTGATGCGA TGCCT                      345

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(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262

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CGGTCTCTAG CGTGCTGGCT AAGATTGAGT CTCTTTAAGG GGATAATCAT GTTCGATTCA      60
ATCGTTTATT TTTTCAATAA GAGCGGGTTT GTTACCACGC TTGTTTTAGT TTGGATTTCG      120
CTTTATTTGG TGATGACTTT ATGGGTCTTT TTGTATAAAA GCATTGTATT AAAGATTGAA      180
CTCAGGCGCG AGATGCAATC TTTGTCTAAC ATTCTTAATG GAGCGCAAGA CGCTCAGAGC      240
ATTTTATGTT TAATAAAAAA AGAAATGATG AGACCAAAAG GTATTCTAAT GAATTGTTGC      300
AGGGCTTGGA AACACCAGGT TCTTAAGCAA AGCAGCAGAG GTTTAGTGGT GTTGAGCATT      360
ATCTCTTCTA CAGCCCCCTT TATTGGTTTG TTTGGGACGG TAGTTGAAAT TTTAGAAGCG      420
TTTAACAATT TGGGCGCGTT AGGTCAAGCT TCTTTTGGAG TGATCGCACC CATTATTTCT      480
AAGGCGCTTA TCGCCACCGC TGCAGGGATT TTAGCAGCCA TTCCAGCCTA TTCTTTTCTAC      540
TTGATCTTAA AGCGCAAGGT GTATGATTTA TCGGTTTATG TGCAGATGCA AGTGGATATT      600
TTGTCTTCTA AAAAAA                                     615

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(2) INFORMATION FOR SEQ ID NO:1263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

902

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263

AAGGTTTTTA TGAATTACGA TAACTATTGG GATGAGGACA AACCAGAACT CAATATCACG	60
CCTTTAGTGG ATGTGATGCT TGTTTTATTG GCTATTCTTA TGGTAACGAC GCCCACTCTC	120
ACCTATAAAG AAGAGATTGC CTTGCCCTTCT GGTTCAAAAA CTGCTAGAGC CACTCAAGAT	180
AAAGTGATAG AGATACGCAT GGATAAAGAC GCAAAAATCT ATATAGATAG TCAAACCTAT	240
GAATACAACCT CTTTCCCGGA CACTTTCAAT TTGCTTTCTA AAAAATACGA TAAAGATACT	300
AGGGTGAGTA TCCGTGCGGA CAAGCGATTG ACCTATGACA AAGTGATTTA TTTGTTAAAA	360
ACGATTAAAG AAGCGGGGTT TTGAAAGTT TCTTTAATCA CAAGTCCT	408

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264

AAAGTAGGGC CAATTTGCAT GAGTAAGAGC GCGATTTTGG TTCTTTCTGG CTTTTTAGCG	60
TTCTTGCTCT ATGCTTTGTT ATTATATGGT TTGTTGTTAG AAAGGCATAA TAAAGAAGCA	120
GAGAAAATCC TTTTAGATTT AAATAAAAAG GACGAACAAG CCATTGACTT GAATTTAGAA	180
GATCTGCCAA GCGAGAAAAA GAATGAAAAA ATTGAAAAAG TAACGGAAAA ACAGGGCGAT	240
TTTTTAGAGC CTAAAGAAGA ACCCAAAGAA GAGCCTGAAG AAAGCCTTGA AGATATTTT	300
TCTTCACTCA ATGATTTTCA AGAAAGACAG ACAAAAACGC TCAAAAAGAC GAGCAAAAAA	360
ATGAACAAGA AGAACAAAGG CGTT	384

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

903

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265

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GGAAGAACAA TGAAATATTT ATGGCTTTT TTAATATACG CTATAGGGCT TTTTGCAACA      60
GATAAAACGC TAGATATTAT TAAAACCATT CAAAAACTTC CTAAGATTGA AGTGCGCTAC      120
TCCATAGATA ACGATGCCAA TTACGCTTTA AAATTGCATG AAGTCTTAGC GAACGATTTA      180
AAGACTAGCC AGCATTTTGA TGTTCCTCAA AACAAAGAGC AAGGTGCTAT CAATTACGCA      240
GAACTCAAGG ATAAAAAAGT CCATCTTGTA GCGCTTGTA GCGTGGCGGT AGAAAACGGC      300
AATAAAATTT CACGATTAAA ACTTTATGAT GTGGATACAG GAACGCTCAA AAAGACTTTT      360
GACTACCCCA TTGTAAGTTT AGATCTATAC CCTTTTGCAG CGCACAACAT GGCCATTGTG      420
GTGAATGATT ATTTAAAGC CCCTTCTATC GCTTGGATGA AGCGCCTGAT TGTTTTTCT      480
AAATACATTG GACCAGGAAT CACAAACATC GCACTAGCGG ATTATACGAT GCCTTATCAA      540
AAAGAAATCA TCAAAAACAA CCGACTCAAT ATTTTCCCA AATGGGCGAA CGCTGAGCAA      600
ACGGAGTTT ATTACACGCA GATGGCGGAA AAACGCCCAT GGT      645

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(2) INFORMATION FOR SEQ ID NO:1266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266

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TTCCTGAGGG GGAAGTTTAT ACAGGAGAGG TTAAGAGCGT TGTGTGCGCA AGGAGTGGA      60
GGGGAATTTG GGGTGCTTTA TGGGCATAGC AACATGATCA CCTTGCTTCA GGCGGGAGTG      120
GTTGAGATTG AAACCGAAAA CCAAAAAGAG CACATTGCTA TCAATTGGGG TTATGCAGAA      180
GTTACTAATG AACGGGTGGA TATTTTAGCC GATGGAGCGG TCTTTATTAA AAAAGGATCA      240
GATGACAGAG ATGATGCTAT CTCTAGGGCT AAAAAGCTT TAGAGGACGC AAGCTCTGAC      300
AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG ATTGAGTCTC TT      342

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(2) INFORMATION FOR SEQ ID NO:1267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

904

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267

AAGCTTAGCA TGAGAGCGAT CGCTATTGTT TTAGCCAGAA GTTCCAGTAA AAGGATTAAG	60
AATAAAATA TGATTGATTT TTTCAATAAA CCCATGCTCG CTTACCCTAT TGAAACAGCA	120
CTAAATCCA AGCTCTTTGA AAAAGTGTTT ATCTCTAGCG ATAGCATGGA GTATGTCAAT	180
TTAGCCAAAA ATTATGGGGC GAGTTTTTTG AATTTACGCC CTAAAAATTT AGCAGACGAG	240
CAGGGCCACG ACTTTAGAAG TGATGGCCTA TCACATGAAA GAATTAGAAT TAAAAGA	297

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268

ATCCCTCCGA GCACACCATT TCTTAACATT CTGCATGTTT TTAAACATTA TCGCTCCCAT	60
TATGGTAAAA TAAATACTTG CTTAAACACG CTAGGAGATT TGATTTTGGC ATTACCCGTT	120
TATTATGATA AAGACATTGA TTTAGGCGTT ATCCAATCCT TACAAGTGGG CATTATTGGC	180
TATGGCGTGC AAGGAGAGGC TCAAGCACTC AATTTGAGGG ACTCTAAAGT GAAGGTGCGT	240
ATTGGCTTGT ATCAAGGGAG TTTGAGCGTT TCAAAAGCAA AAAAAGAGGG CTTTGAGGTG	300
CTAGGAGTCA AGGAATTAGT CCAACAATCT GATGTGATCA TGGCGTTACT TCCGGATGAA	360
TTCATATAAG AAGTGTTAGA AAAAGAAGTG ATCCCTTTTT TAAAAGAGGG GCAAATTATA	420
GGCTTTGCTC ATGGTTTTAG CGTGCATTTT AATCAGGTTG TTCTCCCAAA AGGCGTGGGC	480
GCGATTTTAG TCGCACCAA AGGGCCCCGG AGCGCTTTAA GAGAAGAATA CCTTAAAAAT	540
AGGGGTTTAT ACCATCTAAT CGCCATAGAG CAAGAAAGCT CAATTCATAA CGCTAAAGCG	600
GTGGCTTTAA GCTATGCTAA AGCGATGGGT GGGGGGAGAA TGGGGGTTT AGAAACGAGT	660
TTTAAAGAAG AATGCGAGAG CGATTTATTC GGCGAGCAAG CGGTCTTG TG CGGGGGGT	720
GAAGCGATCG TAAGATGGG GTTTGAAACT TTAATCAAGG CAGGATAC	768

(2) INFORMATION FOR SEQ ID NO:1269:

SUBSTITUTE SHEET (RULE 26)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269

CAGACGAGCA	GGGCCACGAC	TTTAGAAGTG	ATGGCCTATC	ACATGAAAGA	ATTAGAATTA	60
AAAGATGAAG	ACATTGCGTG	TTGTTTGTAT	GGCGTTTCAG	TATTTTACAC	AGAAAAGCAT	120
TTACAAAACG	CTTTTGAAAC	TTTAAACAA	AATCAAAATA	CGGATTATGT	TTTCACATGC	180
TCTCCCTTTA	GCGCTTCGCC	TATCGTTCTT	TTAGCCTTGA	AAACGGCGTT	CAAATGGCTT	240
TTAAAGAGCA	TTCAAACACG	CGCACGCAAG	ATC			273

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270

ATGAAAAGCG	ATAAACCCCTT	TTTAGAACGC	TATTTTATG	ACCCCACTCT	TTTGCAAAAG	60
GGGTTGATTT	TCGCGCTCTA	TCCTTTTTCT	TTAATCTATC	AATGTATTGC	CACAATTAAA	120
CGAAAACCG	CTAAAAGCA	TGATTTTAAA	ATCCCCATTA	TCAGCATAGG	CAACTTGATC	180
GCTGGGGGAA	GCGGTAAAAC	GCCCTTCATT	TTAGAAATCG	CTCCAAGATA	CCAAGAAGTG	240
GCGGTTGTTT	CTAGAGGGTA	TCAACGGGAT	TCTAAAGGTT	TAGTGGTGGT	GAGCGTTAAA	300
GGAAACATTT	TAGTTCCTCA	AAAAACAGCG	GGCGATGAAG	CCTATCTTTT	AGCCTTAAAT	360
CTAAAACAAG	CGAGCGTGAT	TGTGAGCGAA	AAAAGGGAGC	TAGGCGTTTT	AAAAGCCCTT	420
GAATTAGGAT	CAAAGATCGT	GTTTTTAGAC	GATGGTTTTA	GGTTTAATTT	CAACCAATTC	480
AATGCGCTTT	TAAAACCCAA	AGTCCCCCCC	TACTACCCCT	TTTGTGTTCC	TAGCGGGTTG	540
TATAGAGAAA	ATATTAAAAG	CTATAAGAA	GCCCATTTAG	TCATTACAGA	AGATAAGGAT	600
TATCAAAGAA	TCACCTCTAT	CACTAACCCC	ACCAAACGCA	TGCTTTTAGT	AACGGCTATC	660
GCTAACCCCTA	GCAGGCTTGA	TGCGTTTTTA	CCCAAAGAAG	TGGTTAAAAA	ATTGTATTTT	720
AGAGACCATG	CCCCTTTGA	TTGAAGCTT	TTAGAAAAAG	AGTTTTATCA	AAATAACGCC	780
ACCTCCTTAT	TGGTTACTTC	AAAAGATCTC	GTCAAATTAC	AAGATTGCAA	ATTGCCTTTA	840

SUBSTITUTE SHEET (RULE 26)

906

AGCGTATTGG ATTTAAACT AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT 900
 ATCCTTTCTT ATCCTTGTA TATAAAAGAA CATCTA 936

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271

AAAGTGTGT	GGGTGCTATA	TTTTTAACC	AGTTTATTTA	TTTGCTCTTT	GATTGTTTTG	60
TGGTCTAAAA	AATCCATGCT	CTTTGTGGAT	AACGCTAATA	AAATCCAAGG	CTTCCATCAT	120
GCAAGAACCC	CACGAGCCGG	GGGGCTTGGG	ATCTTTCTTT	CTTTTGCGTT	GGCTTGTTAT	180
CTTGAACCTT	TTGAGATGCC	TTTAAGGGG	CCTTTTGTTT	TCCTAGGGCT	ATCGCTAGTG	240
TTTTTGAGCG	GTTTTTTAGA	AGACATTAA	CTTTCATTAA	GCCCCAAAT	ACGCCTTATT	300
TTGCAAGCTG	TAGGGGTCGT	TTGCATCATT	TCATCAACGC	CTTTAGTGGT	GAGCGATTTT	360
TCGCCCCTTT	TTAGCTTGCC	TTATTTTCATC	GCTTTTTTAT	TCGCTATTTT	TATGCTGGTG	420
GGTATCAGTA	ACGCTATTAA	TATCATTGAC	GGGTTTAACG	GGCTTGCATC	TGGGATTTCG	480
GCGATCGCGC	TTTTAGTCAT	TCATTATATA	GACCCTAGCA	GTTTGTCTTG	TTTGCTCGCT	540
TACATGGTGC	TTGGGTTTAT	GGTGTTAAAT	TTCCCTTCAG	GAAAGATTTT	T	591

(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272

CAGTTTGTCT	TGTTTGCTCG	CTTACATGGT	GCTTGGGTTT	ATGGTGTTAA	ATTTCCCTTC	60
AGGAAAGATT	TTTTAGGCGA	TGGGGGGGCG	TATTTTTTGG	GTTTGGTGTC	CGGGATTTCT	120
CTCTTGCAAT	TGAGTTTGGA	GCAAAAAATC	AGCGTGTTTT	TTGGGCTCAA	TTTAATGCTT	180

SUBSTITUTE SHEET (RULE 26)

907

TATCCGGTCA TAGAGGTGCT TTTTAGTATC CTTAGGCGCA AAATAAAACG CCAGAAAGCC	240
ACCATGCCGG ATAATTGCA TTTGCACACC CTTTTATTTA AATTCTTGCA ACAACGCTCT	300
TTCAATTACC CTAACCCCTT ATGCGCGTTT ATCCTTATTC TATGCAACCT GCCTTTTATT	360
TTAATAAGCG TTTTGTTCG CTTGGACGCT TATGCGCTCA TTGTGATTAG CCTAGTCTTT	420
ATCGCATGCT ATTTAATAGG CTATGCTTAT TTGAATAGGC AAGTTTGCGC TTTAGAAAAG	480
CGGGCGTTT	489

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273

ATGAATAAAA CCATAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA	60
AAAGTGATCG CAAGCGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA	120
TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA	180
GACTGCGCGA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTTT ATGGCTCAAC	240
AGCGTGGAAT ATAACGCGCA AATGTCCAAG	270

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274

GTCAAAAAGT CAAATAACAT GGTAGTAGAA TTAAAAACA TTGAAAAGAT TTATGAAAAC	60
GGGTTTCATG CTCTAAAAGG CGTGAATTG GAATTGAAAA AAGGCGATAT TTTGGCGCTG	120
ATAGGCTATT CAGGGGCGGG GAAATCCACG CTCATTGCTG TGATCAATTG TTTAGAGCGC	180
CCCAGTTCTG GCGAAGTTTT AGTCAATGGG GTCAATCTGT TAAACTTAAA GCCTAAAGAA	240

SUBSTITUTE SHEET (RULE 26)

908

TTGCAAAAAG	CGCGCCAAAA	AATAGGCATG	ATTTTCCAGC	ATTTCAATTT	ATTGAGCGCT	300
AAAAACGTGT	TTGAAAACGT	CGCTTTCGCT	CTAGAAATCG	CCCGATGGGA	AAAAACTAAG	360
ATTAAATCAA	GGGTGCATGA	ATTGTTGGAA	TTAGTGGGGT	TAGAAGATAA	AGTGCATTTT	420
TATCCTAAAC	AGCTCAGCGG	CGGGCAAAAA	CAACGAGTGG	CGATCGCTAG	GAGTTTAGCG	480
AATTGCCCTA	ATTTGTTGCT	TTGCGATGAA	GCCACATCCG	CTTTGGATTG	TAAAACCACG	540
CATTCTATTT	TAACGCTTCT	AAGCGGCATT	CAAAAAAAGT	TTGATTGAG	CATCGTTTTC	600
ATCACACACC	AGATTGAAGT	GGTTAAAGAA	TTGTGCAATC	AAATGTGTGT	GATCAGCAGC	660
GGCGAAATCG	TAGAAAGAGG	CTCGGTGGAA	GAAATTTTGG	CTAACCCCTAA	ACATGCTGTT	720
ACTAAAGAAT	TGCTTGGCAT	CAAAAACGAA	CATGCGGATC	AAAAATCGCA	AGACATTTAT	780
CGCATCGTGT	TTTTAGGGGA	GCATTTAGAC	GAGCCGATCA	TTTCTAATTT	GATCAGGCGT	840
TTTAAATAA	GACGT					855

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275

TTATTTTGCT	CCTGCCTTTA	TCAGCGCTTT	TTGATTGGCA	CAAGCATTTG	ATCTAGCGCG	60
AGCATTATCC	CGTTAGCCAT	TTCGGCCATT	CCTTTTGTG	TAAAGCTTTT	TGAAAATTCT	120
TTAATGGAAG	TAGAGCATGG	CAAGATTGAA	ACCACTTTAA	GCTTGGGGGC	GTCTCATTTG	180
GAAGTCATTA	AAATGATGCT	TTTAGAGAGC	CTGCCTTCTT	TAGTGAATAA	TATCACCATC	240
ACTTTAATTT	CTCTAATAGG	CTATTGCGCT	ATGGCTGGAG	CGTTAGGGGC	TGGGGGATTG	300
GGGGATTTAG	CCATTAGGAT	TGGCTATCAA	AGTTATAGGG	GCGATGTGCT	TTTTTATGCG	360
GTGGTCGTGA	TCATCGTTT	AGTGCAAATC	ATTCAAAGCG	CGGGGGATTA	TGTGGTGAAA	420
CGCTTGAGAA	AGAATAAGTA	T				441

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276

TCTTATTTTT	GTATAATCT	TAGGTTGTTA	AGTTTAGTTA	AAGGGAAAAC	CATGCTCCGC	60
TCTCTCTATA	GTGCCACTTC	AGGGATGCTC	GCCCAACAAA	CGCACATTGA	CACCACTTCA	120
AACAACATCG	CCAATGTCAA	TACCACCGGG	TTTAAAAAAT	CTCGCGCGGA	TTTAAACGAC	180
TTGTTTATACC	AAGCGATGCA	ATACGCCGGC	ACCAACACAA	GCAACACGAC	TTTATCGCCA	240
GATGCGATGG	AAGTGGGCCT	TGGCGTACGC	CCTAGTGC GA	TTACCAAAT	GTTTTCGCAA	300
GGCAGCCCTA	AAGAAACGGA	GAATAATTTA	GATATTGCTA	TTACAGGTAA	AGGCTTTTTT	360
CAAGTCCAGC	TTCCTGATGG	CACTACCGCT	TACACAAGGA	GCGGGAATTT	CAAGCTAGAC	420
GAGCAGGGCA	ATCTTGTAA	AAGCGAGGGC	TATCTCTCTA	TCCCTCAAAT	CACTTTACCC	480
GAAGACACCA	CGCAAGTGAA	TATCGGTGTG	GATGGCACGG	TGAGCGTGAC	TCAAGGCTTG	540
CAAACGACTT	CTAACGTGAT	CGGGCAAATC	ACTTTGGCTA	ATTTTGTCAA	TCCGGCGGGG	600
CTTCATTCTA	TGGGGGATAA	TTTGTTCCTC	ATCACCAACG	CTAGCGGCGA	TGCGATTGTG	660
GGCAACCCGG	ATTCTCAAGG	CTTAGGCAAG	TTAAGGCAAG	GCTTTTTTGA	GCTTAGTAAC	720
GTGAGATTGG	TAGAAGAAAT	GACAGATCTA	ATCACCGCTC	AAAGGGCTTA	TGAAGCCAAT	780
TCTAAAAGCA	TTCAAACCGC	TGATGCCATG	CTCCAAACAG	TCAATTCCT	CAAACGC	837

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277

AAATGGCGCA	ACTCATCAAG	CGATAAAATG	GCTAAAAAGA	AAATTGCGAT	CAGCTGTGGG	60
GATATTCAAG	GCGTAGGCTT	AGAATTGATC	TTAAAAAGCC	ATAAGGAAGT	GAGTGCACCT	120
TGTGAGCCGT	TGTATCTCGT	TCATAGCGAA	CTTCTAGAAC	GAGCCAATCA	ATTGCTTGAT	180
AACGCTTATG	AAACTAAAC	GCTTAATGCG	ATCGCTATTG	ATGCCCTTTT	ACCTTTATTA	240
AACTCTAGCA	CGATAGGCAA	AGTCAGCACT	CAAAGCGGGG	CGTATAGCTT	TGAGAGTTTT	300
AAAAAGGCTT	GCGAGTTGGC	GGATAGTAAA	GAAGTGGATG	GCATTTGAC	TTTGCTTATC	360
AACAACTCG	CATGGCAACA	AGCTCAAATC	CCTTTTGTGG	GGCATAACCGA	TTTTTTGAAA	420
CAACGCTACA	AAGATCATCA	AATTATTATG	ATGCTTGGGT	GTTCAAAACT	CTTTGTGGGG	480
CTATTTAGCG	ACCATGTGCC	TTTAAGCGCG	GTTTCTCAAC	TCATTCAAGT	GAAAGCGTTA	540
GTTAAGTTTT	TATTAGCGTT	TCAAAAAAGC	ACTCAAGCCA	AAATCGTTCA	AGTGTGTGGT	600
TTCAACCCCC	ATGCGGGCGA	AGAGGGATTG	TTTGGGGAAG	AAGATGAAAA	GATTTTAAAA	660
GCCATTCAAG	AGAGCAACCA	AACGCTAGGT	TTTGAATGCT	TTTTGGGGCC	ACTGCCCGCT	720
GATAGCGCTT	TTGCCCCCAA	TAAACGCAAA	ATAACCCCTT	TTTATGTGAG	CATGAGCCAT	780
GATGTAGGGC	TAGCCCTTTT	AAAAGCGCTC	TATTTTGATG	AAAGCATCAA	TGTGAGTTTG	840
AACGCTCCCA	TTTACGCGC	TTCCACTGAC	CACGGCACGG	CGTTTGATAT	TGCTTATCAA	900
AATAAGGCGA	ACCATAAAAG	CTATTTGAAC	GCGATCAAAT	ACTTGGCT		948

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs

SUBSTITUTE SHEET (RULE 26)

910

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278

CAAGGTATAA	TTCAAGCAAA	AACACCACCC	AAAGATAAAG	ACATGATTTT	AAGCATTGAA	60
AGTTCTTGCG	ATGACAGCTC	TTTAGCCCTT	ACAAGAATAG	AGGACGCCAA	GCTCATCGCT	120
CATTTTAAAA	TCTCTCAAGA	AAAGCACCAC	AGCTCTTATG	GGGGCGTTGT	GCCTGAGATT	180
GCATCGCGCC	TGCATGCTGA	GAATTGCGCG	CTTTTATTAG	AACGCGTTAA	AATAAGCTTG	240
AATAAGGATT	TTTCCAAAAT	TAAAGCCATC	GCTATCACTA	ATCAGCCAGG	TTTGAGCGTT	300
ACTTTAATAG	AGGGTTTGAT	GATGGCAAAA	GCCTTGAGCT	TGTCCTTGAA	TTTACCCTTG	360
ATTTTGGAAG	ATCATTTGAG	AGGGCATGTG	TATTCGCTCT	TTATCAATGA	AAAACAAACC	420
CGCATGCCCT	TAAGCGTGTG	GCTAGTCTCT	GGGGGGCATT	CTTTAATTTT	AGAGGCTAGA	480
GATTATGAAG	ACATTAAAAT	CGTTGCCACG	AGTTTAGACG	ATAGCTTTGG	GGAGAGTTTT	540
GATAAGGTTT	CAAAAATGCT	TGATTTAGGC	TATCCAGGAG	GCCCCATAGT	GGAAAAATTA	600
GCCCTTGATT	ATGCACACCC	AAACGAGCCT	TTAATGTTCC	CTATCCCTTT	AAAAAACAGC	660
CCGAATTTGG	CTTTTAGTTT	TTCAGGTTTA	AAAAATGCGG	TGCGTTTGGA	GGTTGAAAAA	720
AACGCCCATTA	ATTTGAACGA	TGAGGTAAAA	CAAAAGATTG	GCTATCATTT	TCAAAGCGCG	780
GCTATCGAGC	ATTTAATCCA	GCAGACTAAA	CGCTATTTTA	AAATCAAACG	CCCTAAAATT	840
TTTGGCATTG	TGGGGGGAGC	GAGCCAAAAT	CTAGCCTTAA	GAAAGGCGTT	TGAGGATTTG	900
TGTGCTGAGT	TTGATGCGGA	GCTTGTTTTA	GCCCCCTTAG	AATTTTGCAG	CGACAATGCC	960
GCCATGATAG	GGCGATCAAG	CCTAGAAGCT	TATCAAAAAA	AGCGCTTTAT	CCCTTTAGAA	1020
AAAGCCGATA	TTTCGCCAAG	AACGCTGTTA	AAAAATTTTG	AG		1062

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 768 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279

AGGAATAATA	TGGCATACAA	ATATGATAGA	GACTTGGAAT	TTTTAAAGCA	ACTGGAATCT	60
AGTGATTTAT	TGGATTTGTT	CGAGGTGCTT	GTYYYYGGTA	AAGACGGCGA	AAAAAGACAC	120
AATGAAAAAC	TCACAAGCTC	CATAGAATAC	AAAAGGCATG	GCGATGATTA	CGCTAAATAC	180

SUBSTITUTE SHEET (RULE 26)

911

GCAGAAAGAA	TCGCTGAAGA	GTTGCAATAC	TATGGGAGCA	ATAGTTTTGC	GAGTTTCATT	240
AAAGGTGAAG	GAGTCTTATA	CAAAGAGATT	TTATGCGATG	TGTGCGATAA	ATTAAAGGTC	300
AATTACAACA	AGAAAAGTGA	AACGACTTTA	ATTGAACAAA	ACATGCTTTC	TAAAATCTTA	360
GAAAGAAGCC	TAGAAGAAAT	GGATGATGAA	GAAGTGAAAG	AAATGTGCGA	TGAATTGTCC	420
ATAAAAAACA	CGGACAATTT	GAACAGACAA	GCCTTAAGCG	CGGCGACTTT	AACGCTGTTT	480
AAAATGGGAG	GCTTTAAATC	TTATCAATTA	GCTGTCATTG	TTGCGAATGC	GGTTGCAAAA	540
ACCATTCTAG	GGCGTGGTTT	ATCGCTTGCG	GGCAATCAAG	TGCTTACAAG	AACTCTGAGC	600
TTTTTAACAG	GCCCTGTTGG	CTGGATCATT	ACAGGCGTAT	GGACAGCGAT	TGATATGCA	660
GGGCCGGCTT	ATAGGGTAAC	CATACCGGCA	TGCATTGTGG	TCGCCACTTT	ACGCCTAAAA	720
ACGCAACAAG	CCAATGAAGA	TAAGAAGTCG	TTGCAAATAG	AATCCGTT		768

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280

GTTATAATAT	TTTTGCTATT	GTTTTTTT	GGAAATAAAG	TTTTCAGTAT	TTATTGCTT	60
TTAGAGTCAT	TTTTGTGGGT	AATATTGACC	ACTTGGTGTT	GTTTGTCAT	GCATGAAGAT	120
CAGAGACAAA	AAGACATGGA	ACAACCTATC	AATGGGATTG	ATAGGATTAT	TAAAGCAAAT	180
TCCGGTAAAT	CTTTACACCA	AGAAACACAA	CAAGCAAATA	AAACCGATAA	AGCATGGGAT	240
TTGCGGGCTA	ATGTTTTTCT	CATTGGTCTG	GTGTTTTTGG	CTGTTTTTCA	CATGATCAAG	300
CGA						303

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281

SUBSTITUTE SHEET (RULE 26)

912

GCGGTGAAAA AAGTAGAATC CATGAATGTG GTGCCTTTCA TTGACATCAT GCTTGTGTTG	60
TTAGTGATCG TGCTCACAAC GGCCTCTTTT GTGCAAACTT CAAAGCTTCC TATTAGCATT	120
CCTCAAGTGG ATAAGGATAG CACTGATTCT AAAGATGTGT TGGACAAAA ACAAGTTACG	180
ATCGCTATTT CTAATAAGGG TTCTTTTAT TTTGACGATA AAGAAATCAG CTTGAAAAAT	240
TTAAACACA AGGTTTCCAC TTTGGCTAAA GACACCCTA TTGTCTTGCA AGGCGATAAG	300
AAAAGCAATT TGGACAACTT TATCAAAGTG GTGGATTAT TGCAACTAAC AATC	354

(2) INFORMATION FOR SEQ ID NO:1282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282

CTACACAGAC AGGCGCAAGT TAGAATTAGC CTTACACAAA CGACGACTTT AGTGCCCACT	60
ATTGGCTCAA ACGCCCTTA TATCGGTCTT TTAGGGACGG TTATGGGGAT CATGCTCACC	120
TTTATGGATT TAGGCTCAGC TTCTGGCATT GACACTAAGG CGATCATGAC TAATTTAGCC	180
CTTGCTTTAA AAGCGACCG CATGGGGTTA TTGGTAGCGA TCCCTGCGAT TGTGATTAT	240
AACTTGTTAG TGAGAAAAAG CGAGATTTTA GTTACCAAAT GGGATATTTT CCACCATCCG	300
GTTGATACGC AATCCCATGA GTTTATAGC AAAGCC	336

(2) INFORMATION FOR SEQ ID NO:1283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283

AACCATAAGA TTAGGGGTTA TGAAAAACGC ATGGCATTAG ACAAAGGAT TTGGATGCAT	60
TTTGATCTTT TGCCTTTGT GTTTATCATC CCCTGTTGG TGGTTTCTTT TTTGTTGATT	120

SUBSTITUTE SHEET (RULE 26)

913

TTTGAGAGTA GTGCGGTTTT GAGCTTGAAG CAAGGGGTTT ATTATGCCAT AGGGTTTCTT	180
CTCTTTTGGG TAGTGTTTTT TATCCCTTTC AGGAAACTCG ATCGGTGGCT CTTTGCCTT	240
TATTGGGCGT GCGTTATTTT ATTAGCGTTA GTGGATTTTA TGGGATCGAG CAAGCTTGGA	300
GCGCAGCGAT GGCTAGTCAT TCCTTTCACT TCTATCACCT TACAGCCTAG CGAGCCTGTG	360
AAAATCGCTA TTCTTTTATT GTTGGCGCGA TTTGATCAAA ATCAACCCAC CTCCTTT	417

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284

TTTTGTGGGA CACTAAAGGC ATTGAAGATA AAGATTACCA CGACACCATG CAAAGCATT	60
AAAAAGAAAT GGAAGATTCT TTTAAACAC TTGATGAAAA AGAAGCCATT GATGTGGCGT	120
ATCTGTGCGT TAAGGAGACT TCTTCTAGGG TTCAAGAGAG AGAGAGAGTT ATTAAGCTTC	180
GCTAAACATT GGAATATCCC AACGATTGTC GTTTTCACAC ACACTCAAGC CGAAGCCGGC	240
GATGCGTTTG TCCAAGAAAC TAAAGGGATC ATAGACGAAG AATGGGGGTT TAAAGGTTTT	300
GTCAGAGCCT ATGTGAGGGT CAATTCCGTT GCCTTTTCAT TTAGGGGGTT GAAAGTCCCT	360
GTTGAAGGTT TAGAAGAATT GGTAGATGAA ACGAAAAAAT GCCTTTCAGA CGCTGAAAAA	420
AATAAGAAAA GGCATTTCCT GAGTATTCAA AGAGTTAAGA TTCAAGAAAG AAAACAGGCT	480
ATGATAGAGG AATGTAAAAC CATTATCCAT GTTGCATCAG GCGCTGCAGG AGTTGCTGGG	540
CTTATCCCCA TACCTTTTAG CGATGCGCTC GCTATCGCAC CCATTCAAGC AGGGATGATC	600
TATAAATGA ATGACGCTTT TGAATGGAT TTGGATAAAT CTGTGGGCGC GAGTTTGGTC	660
GCAGGATTGT TAGGCGTAAC CGCTGTCCGC CAAGTGGGGA GGACTCTCGT TAATGGTTTC	720
CTTAAATTCA TTCCTGTTGT GGGGAGTGTT GCAGGGGGCG CAACCGCTGC TGTATCACA	780
GAAGGCATTG GGTTCGCTA TTGAAAGTG CTAGAAAAGT GCTTTAATGA TGAGACGGGT	840
GAAGTCAATT TGCCTGGTGA AGTTGGCATG ATCACTTCTC TCTTTAAGGA GAATTATCTC	900
AACTTGATA CAATCAAAA ATTAAAACCA	930

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

914

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285

ATGAGGTCCT	GGATGAAGAA	AAAATACTTC	ACGCTTTTAT	TGCAAAGTAG	TGTGGTATTA	60
GCGGTTTTTA	TAGGGTGTTT	TTCTACCAGG	AATCATACTT	TTTCAGCCCT	TAGTAATCAA	120
GAAAATACAG	ACGATAAGCT	CCCAGTGGTC	CATTCCATTA	AAACGATTAA	CGATGTGAGT	180
TCAGTGGGCT	TTGAATGGTC	TAAAGTCGCT	GACACTTATG	ACATTGACGG	GTTTGTGTTG	240
TATCGTTTGA	AAAAAGACTC	CAAGCTTAAA	AGAATCGCCA	CCATTAAAAA	CCCTTATGCG	300
ACCCACTATT	ATGATGAGGG	GTTAGAAACA	GAGAGTTCCT	ACACTTACCA	ATTAGCCACC	360
TACAAGGGCG	ATAAAATTTT	CAAACCTTCA	GAACCCATTT	TAGTAAAAAC	CTCCTTTATC	420
AATCCTGTAG	AAAGCGTGT	TGCAAGCCTT	GAATACCCCTA	AAAGCGTGAA	AGTCTTTTGG	480
AGCCCGCACC	CAAATCCCAG	CGTTTCTAAA	TACATCATT	AAAGGCAGAA	TAAAGACGGC	540
AAATTTTTAA	ATGTGGGGGC	TGTAAAAAAC	CGCTTATTCG	TGGAGTTTTT	TGATAAAGAT	600
TTAGAGATG	GGCAAAAATA	CCGCTACCAA	ATCATCGCCG	AAAATTTTCAT	GGGGGATAAA	660
TCCAGGCCTA	GCGTGATAGT	GGAGGGGAAA	ACCAAAGACT	TGCCCCAAGA	AATCGCTAAT	720
GTTAGAGTGA	GTCAAAACCT	CACACGACAA	ATTGAATTGA	GTTGGGATAA	ATCCCCAGAA	780
GAAGATGTGA	TAGCTTATCG	CATTTACGCT	TCCAATAACC	GCAACGATAA	ATACAAATTC	840
ATCGCTCAAA	CCACCAACAC	TTCTTATGTG	GATAAGATAG	AAAAAGACAA	TCTCACTCGT	900
TATTATAAAG	TCGTCGCCGT	AGATAAAACG	CATCTTGAAG	GGGCGTTACC	CAAAGAGCCT	960
GCCATGGGTG	AAACCTCTGA	TAGGCCTGAA	GCCCCATCA	TCTACTAAGG	GACTATTCAA	1020
GACTCTTCGG	CCTTGATCCA	ATGGGAAAAC	AACCCAAGCC	CTAAAATAGC	CACTTATGCG	1080
GTGTATCGTT	TTGAAGCCAA	CTCCAAAACC	CCTTTGCGTT	TTGGGAATAT	CACACAAAAC	1140
CAGTTCTGTG	ATAAGGACAT	GAAAGTGGGC	GTGGCTTATC	GCTATCAGGT	GGTGAGCGTG	1200
GATAAAGATG	GTTTAGAGTC	GCACCCAAGC	AAAGAAGTGC	GTTTGTTTTT	AGAGCGC	1257

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286

CTTAAAAACA	CTCTAAAAGG	GTTATTGATG	CTGGATTTTG	ATTGTTTCT	TTTTGGCGCG	60
ACTGGGGATT	TAGCCATGCG	AAAGCTCTTT	GTTTCGCTTT	ATGAAAATTTA	TATTCATTAT	120
GGTTTTAAAA	ACGATTCTAG	GATTATCGCA	TCGGGGCGTA	AGGAGCTATC	CAATGAAGAG	180
TTTTTAGCGC	TTCTTTGTGA	AAAAACACAA	CTGCATTCAA	GAGAAAAGGG	TGAGGAATTT	240
TTAACCCATA	TCAGTTATTT	GCGCGTCCGT	TTGGATAACC	CTAAAGACTT	TGAAGAATTG	300
AGTAAAATCG	CCACAAACAA	TAAGCCCTTG	ATTTTCTACT	TTTCTATCTC	CCCTAGTTTT	360
TTTGCAACGA	CCGCTCAAAA	TTTAGCCCAA	AACGCGCTCA	ATCAGCTAA	CACTCGTTTG	420
ATTCTAGAAA	AGCCTTTAGG	GCATGATTTA	AAGACTTGTA	AAGAGATTTT	CCAAAGCATT	480
AGCGCTTTTT	TTAAAGAAGA	ACAAATTTTT	AGAATCGATC	ATTATTTAGG	GAAAAAGGGC	540
GTTCAAAATA	TCCTTGAATT	GCGCCTGAAT	AACCTTATCT	TAAACATTTT	ATGGGATCAA	600
ATCAGCGCGG	TTGAAATCTG	CGTGTATGAG	ACTTTAGGGG	TGGAAGAAAG	GGGCGAATTT	660
TACGATAAAA	TCGGGGCTTT	AAGGGATATG	GTTCAAAACC	ATCTCTTGCA	AGTTTTATCC	720
CTTATCGCTA	CAGATTTACC	CAACGATTTA	AAAGATTTGA	GGCAAGAAAA	ATCAAAGTTT	780

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287

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GGCATGGTTA AACACTATCT TTTCATGGCG GTTTCGCAGG TCTTTTCTC CTTCCTTTTA      60
GTGCTGTTTT TTAATCAGTA TTGCAAGCGT AACGCTCGTG      120
ATTAAAGTGA GCTTTTIGGA TCTGGTGCAA CTCTTTTGT ATTCTTGCC AGGAACCACT      180
TTTTTTATTT TGCCGATCAC TTTTITGCG GCTTGCCTT TGGGGCTTTC AAGGCTTAGC      240
TATGACCATG AATTGTTAGT GTTTTCTCT TTAGGGGTTT CGCCTAAAAA AATGACTAAA      300
GCGTTTGTGC CTTTAAGTTT GTTAGTGAGC GCGATTTTAT TAGCGTTTTC GCTCATCTTA      360
ATCCCCACTT CTAAGAGCGC TTATTACGGG TTTTTCGTC AAAAAAAGA CAAGATTGAC      420
ATTAACATCA GAGCGGGTGA ATTTCGGCAA AAATTAGGCG ATTGGCTCGT GTATGTGGAT      480
AAGACTGAAA ACAATTCCTA TGATAATTG GTGCTTTTTT CTAATAAAG TCTCTCTCAA      540
GAAAGCTTTA TTTTGGCTCA AAAAGGCAAT ATCAACAATC AAAACGGCGT GTTTGAATTG      600
AATTGTATA ACGGCGATGC GTATTCTACT CAAGGCGATA AAATGCGTAA GGTTGATTTT      660
GAAGAATTGC ATTTGCGCAA CAAGCTCAAG TCTTTCAATT CTAATGATGC GGCTTATTTG      720
CAAGGCACGG ATTATTGGG TTATTGAAA AAAGCCTTG GTAAAAACGC TAATAAAAT      780
CAAAAACGCC GTTTTCTCA AGCGATCTTA GTTTCCTTG TCCCTTTAGC GAGCGTGT      840
TTAATCCCCT TATTGGCAT CGCCAACCCG CGATTCAAAA CGAATTGGAG TTATTCCAT      900
GTCCTTGGAG CGGTGGGGT TTATTTTATA ATGGTGATG TGATTCTAC GGATTGTTT      960
TTGATGACCT TTTTCTTCCC CTTTATTGG GCGTTTATT CTTATTTATT GTTTAGAAAA     1020
TTCATTTTAA AGCGTTAT

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(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288

ATCTTAATTG	AAGGGGTGTT	CATGCCTAAG	CATTCTTTAG	AACAAATCAA	AGAAAAAATT	60
ACAGAGCGTA	GCAAAAAAAC	CAGAGAGCTT	TATTTAGAAA	ATACCTTCAA	CCCTAAAAAC	120
CAGCCCAAGA	TTGAGAGCTT	GGGTGCGCG	AATATTGCGC	ATGTTACGGC	GAGCATGCCA	180
GAGCATTTAA	AAATGCCTTT	AGGTTGCGAT	AAAAGAAAGC	ATTTTGGGAT	TATCACCCT	240
TATAATGACA	TGCTTTCAGC	CCACCAACCT	TTTAAAAAAT	ACCCTGATCT	GATTAAAAAA	300
GAGTTGCAAG	AGCATAACGC	CTATGCGAGC	GTCGCTAGTG	GGGTGCCAGC	GATGTGTGAT	360
GGTATCACGC	AAGGTTATGA	GGGAATGGAA	TTGAGCTTGT	TTAGTAGAGA	TGTGATCGCA	420
TTAAGCACCG	CCGTAGGGTT	AAGCCATAAT	GTTTTTGACG	GGGCGTTTTT	TTTGGGCGTG	480
TGCGATAAAA	TTGTGCCAGG	CTTGCTCATA	GGAGCGTTAA	GCTTTGGGAA	TTTAGCGAGC	540
GTGTTTGTGC	CAAGCGGGCC	TATGGTGAGC	GGGATAGAAA	ATTATAAAAA	AGCCAAAGCG	600
CGCCAAAGATT	TTGCAATGGG	AAAGATCAAC	AGAGAAGAGC	TTTTAAAAGT	GGAAATGCAA	660
AGCTATCATG	ATGTGGGCAC	TTGCACTTTT	TATGGCACGG	CTAATTCTAA	TCAAATGATG	720
ATGGAGTTTA	TGGGGTTGCA	TGTGGCCAAT	TCTAGCTTTA	TCAACCCTAA	CAACCCCTTA	780
CGAAAGGTTT	TAGTAGAAGA	GAGCGCTAAA	AGATTAGCGA	GCGGGAAAGT	CCTGCCTTTA	840
GCCAACTCA	TTGATGAAAA	AAGCATTCTT	AACGCTCTTA	TAGGCTTAAT	GGCAACAGGG	900
GGTCTTACTA	ACCACACTTT	GCATTTGATC	GCTATCGCTA	GATCTTGTGG	GGTGATCCTC	960
AATTGGGACG	ATTTTGACGC	AATCTCTAAT	CTCATACCCC	TTTTAGCTAA	AGTCTATCCT	1020
AACGGATCAG	CGGATGTGAA	CGCTTTTGAA	GCGTGTGGGG	GCTTAGCGTT	TGTGATCAAA	1080
GAATTGCTAA	AAGAGGGGCT	TTTATTTGAA	GACACTCATA	CCATTATGGA	TACAGAAACG	1140
CAAAAAGGCA	TGCAAAATTA	CACCAAAACC	CCCTTTTGTAG	AAAACGACCA	ATTGGTGTAT	1200
AAAGACGCTG	TTAGTCATAG	CCTGAATACG	GATATTTTAC	GCCCTGTTAG	TGAGCCTTTT	1260
GCCGCTAATG	GAGGGCTTAA	AATCTTAAAA	GGTAATTTGG	GGCGGGCCGT	GATTAAAAATC	1320
TCAGCCATTA	AAGATGAGCA	TAGGAAAGTT	AAAGCTAGAG	CGATTGTTTT	TAAAACCCAA	1380
AGCGAATTTT	TAGAACGCTT	TAAAAATAAA	GAATTAGAAA	GGGACTTTGT	GGCGGTCTTG	1440
CCTTTCCAAG	GGCCTAAGTC	TAACGGCATG	CCAGAATTGC	ACAACTCAC	CACGAATTTA	1500
GGGGCTTTGC	AGGATATGGG	CTACAAGGTC	GCGCTCGTTA	CGGATGGGCG	CATGAGTGGG	1560
GCGAGCGGGA	AAGTGCCTAG	CGCGATCCAT	TTAAGCCCTG	AGGGGGCGTT	AAACGGGGCG	1620
ATCATTAAAG	TTAAAGATGG	CGATTTGATA	GAATTAGACG	CTCCTAATAA	CGCCTTGAAT	1680
GTGCTTGAAA	AGGATTTTGA	AAAGAGAGGC	ATCAACCCCT	TGTTTTTAGA	AACCTTAGAA	1740
AATTTAGAAA	AGCCTACTTT	TGGGTTGGGT	AGGGAATTAT	TTACAAGCTT	GAGATTGAAT	1800
GCCAATACCG	CTGAAGAGGG	TGGCATGAGT	TTTGGCATAA	AGGTA		1845

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289

AAATATAAAG	GAGATAAAAT	GCAAGATAAA	ATAATAGAAA	TTTTACAAAT	CAGCCCCATT	60
GTCCCTGTGG	TGTTGGTTGA	GAATATAAAA	GACGCTGTGC	CTTTAGCGCA	AAGCCTGATA	120
GAGGGGGGTA	TTCCAATCAT	AGAAGTAACT	TTGCGATCAA	ACTGTGCTTT	AGAGGCCATA	180
GAGCTTATCG	CTAAGAATGT	GCCAAAAATG	CGCGTGGGTG	CTGGCACGAT	ACTCAATCTC	240
ACTCAATTAG	AGCAGGCTCA	AAATAGGGGG	GCAGAGTTTT	TGATTAGCCC	GGGTCTTACG	300
ATAAAGCTTT	TAGAACACGC	AAAGAAAAAA	GACATGCCTT	TAATACCTGG	GGTTTCTAGC	360

917

AGCAGTGAAG TCATGCAAGC TTTAGAATTG GGTATAACG CTTTGAAATT TTTCCCGGCG	420
GAGTATTGCG GGGGCGTTAA ACTTTTAAAC GCTTTTAACG GCCCTTTTAA AGGGGTGAAA	480
TTTGCCCCA CTGGGGGGAT TAGCGCAGAT AACATGCGTT CTTATTTGGC TTTAGAAAAC	540
GTTGTGTGCG TGGGGGGGAG CTGGCTTACC CCTAAAGATT TAATTCAAA CAAAGAGTGG	600
GATAAGATCA CAGAAATTG CAAGAGAGCG TTAGCTTTAA GA	642

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290

AATACCGCTA TTGATCGTT TTTATGGTTT GCTTATGTTT CTATAGGTTT AACTAATTTT	60
GTAGCTGTTG GTTATATGGT ATCGTTGCTT GCGCGCTTA AACGCACCCC TTGCACTAAT	120
CGCTTTTATC TTAAAGCACT ACTATTTGCT ATATTCTATC ATGCAGTAAA TAATTTTCTA	180
ACGCAATGCC CGCCCCATCA AGTCCGGGAG TTTTTTTCAT CACGACATGC ACAGGGATGG	240
AAGCGAGAAA CGCTCCCATG CGCCCTTTCG TTTCAAAACG CGCTC	285

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291

AAGAAAACGC CCCCTATTCT CTGCCGATTG CTCGGATTTT ACATTCTAAA AAAGTTACCA	60
CAGAGGTGTT TTATGCCAAA AACTGAAACT TACCCAAGAC TATTAGCCGA TATTGGCGGC	120
ACAAATGCCG GTTTTGGTTT GGAAGTCGCC CCACGACAGA TTGAATGCGT TGAAGTCTTG	180
AGGTGCGAAG ATTTTGAGAG CTTGAGTGAT GCGGTGCGAT TTTACCTTTC TAAATGCAAA	240
GAAAGCCTTA AACTGCACCC TATTTATGGC TCTTTTGCTG TGGCTACGCC CATTATGGGG	300

SUBSTITUTE SHEET (RULE 26)

918

GATTTTGTCC	AAATGACGAA	CAACCACTGG	ACTTTTTTCTA	TTGAAACGAC	ACGGCAATGT	360
TTGAATTTAA	AAAAACTGCT	TGTCATCAAT	GATTTTGTCTG	CGCAAGCCTA	TGCCATTAGC	420
GCGATGCAAG	AAACGATCT	AGCCCAAATA	GGCGGGATTA	AGTGTGAAAT	CAACGCTCCT	480
AAAGCGATTT	TAGGGCCAGG	AACCGGGCTT	GGGGTAAGCA	CTCTTATCCA	AAACAGCGAT	540
GGCTCTTTGA	AAGTCTTGCC	CGACGAAGGT	GGGCATGTGA	GCTTTGCCCC	TTTTGATGAT	600
TTAGAAATTT	TAGTGTGGCA	ATACGCCCGC	TCTAAATTCA	ACCATGTGAG	CGCGGAAAGG	660
TTTTTGAGCG	GTAGCGGCCT	GGTGTGATT	TATGAAGCCC	TGTCTAAACG	CAAAGGCTTA	720
GAAAAAGTGG	CGAAGTTGAG	CAAGGCTGAA	TTAACCCAC	AAATCATTAG	CGAACGCGCT	780
TTGAATGGGG	ATTACCCTAT	ATGCCGATTG	ACCTTGGACA	CTTTTGTCTC	CATGCTTGGC	840
ACGCTCGCTG	CTGATGTGGC	TCTCACTTTG	GGGGCTAGAG	GGGGGGTGTA	TTTGTGTGGG	900
GGGATTATCC	CACGATTCAT	TGATTATTTT	AAAACTTCGC	CCTTTAGAGC	GCGTTTGTAA	960
ACGAAAGGGC	GATGGGAGC	GTTTCTCGCT	TCCATCCCTG	TGCATGTCGT	GATGAAAAAA	1020
ACTCCCGGAC	TTGATGGGGC	GGGCATTGCG	TTAGAAAATT	ATTTACTGCA	TGATAGAATA	1080

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292

TCCCAGGGAC	TGATTTTTGA	TAAAAAGAAA	CAAAAATTTT	TAAAAGATTT	TAAAGCAGGA	60
GAATTATGT	ATCAATCCCA	TTTCAAACCA	TTAGTAGAAT	TTATAGCCGA	AGAGCTTCTT	120
AAAAACTCGC	GCGCCAAAAT	CATTCAATCA	AAGTGAATA	AAGCCTTAAA	AGTGGTAGAA	180
GAATTACAAA	ATACGATAAA	AACCACGATT	GAAAAACAGA	TCAATCCAGG	GATGAAAGAA	240
ACACAAGACC	CCCAACAAGA	AGCTCGCTTT	AATTTGGATC	GTTCTACAGA	TAAATTTATA	300
TCAGATTTGG	AAAAATCAGC	GTTCAGCAAA	ATCAATCAAT	TCGAATTTAA	TTTTAGAAAA	360
GAAATGCATG	AACGCATTGA	AAGAGGTATT	GGAAATAATG	AATGTAAAGA	AATTTTTGGC	420
AATGAACCTA	AACAAAGAAA	GACAAAATTG	ATTGAAGACA	TAGAACGGCG	GTTCAAAGAA	480
TGCGAGGAAC	AATTCCGTGG	AAGTGTAGGA	AAAAATATTG	AACAACCTGA	AGAAAGAGTT	540
AAAGATTCTC	TAGCGATTAT	AAAACGCATC	AATAACCTTG	GTCCTTAATC	TAATTTCTAAT	600
TTTAATATGG	ATAGCGGCAT	TGATACAATA	GGCTTATTTA	GTTCAATAGG	AGGTTTGGTG	660
TTGCTTCTAT	TGACGCCTGT	AGTAGGTGAG	TTTGCGTTAA	TTGCAGGAGT	GGGTTTAGCA	720
TTAGTGGGGG	TAGGTAAATC	AATATGGAGT	TTTTTTGATT	CAGATTATAA	AAAATCCCAA	780
CAAAGAAAAG	AAGTGGATAA	GAATTTACAT	CAAAATTGCG	AAAAAATGT	GCAGGATGTG	840
AAAAGCCGCA	TTGAAAGTTA	TAAAAATGGT	GCATTGGGAA	TGATTGAAGA	ACTCAACGCC	900
GGTTTTAACA	AACCTTGTGA	TCATTACGAA	CGCATGAAAA	GACAATTGGA	AGAAGCCCAT	960
GAAAAACTAG	GATACATCTA	TAATAGTATC	CATCTTACAA	TATCTAACCG	CCGCATACAA	1020

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

919

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293

AGTGCCTTAT	GGCACAAAGA	CCCCACCACG	ATCAAGCAAT	TTGGCTTAGA	GGCTTTGGAT	60
TTTTTCAAAC	CGCATGAGAT	TGAATTATTG	ATTGTGGCAT	GCAACACCGC	GAGCGCTCTG	120
GCTTTAGAAG	AGATGCAAAA	GTATTCTAAA	ATCCCTATTG	TGGGCGTGAT	TGAGCCAAGC	180
ATTTTAGCGA	TCAAGCGGCA	AGTGGGAAGAT	AAAAACGCCC	CTATTTTAGT	GCTAGGGACA	240
AAAGCGACGA	TTCAATCCAA	CGCCTATGAC	AACGCCCTGA	AACAACAAGG	CTATTTGAAC	300
ATTTTCGATT	TAGCTACTTC	TCTTTTGTG	CCTTTGATTG	AAGAAAGTAT	TTTAGAGGGC	360
GAATTGTTAG	AAACTTGCAT	GCATTATTAT	TTCATCCCT	TAGAGATTTT	ACCCGAAGTG	420
ATCATTTTAG	GTTGCACGCA	TTTTCCCTTA	ATCGCTCAAA	AAATTGAGGG	CTATTTTCATG	480
GGGCATTTTG	CCCTTCCAAC	GCCCCCCTA	CTCATCCATT	CGGGCGATGC	TATTGTAGAA	540
TATTTGCAAC	AAAATACGC	CCTTAAAAAC	AATGCATGCA	CATTCCCTAA	AGTGAATTT	600
CATGCGAGCG	GCGATGTGAT	CTGGCTAGAA	AGACAAGCTA	AAGAATGGCT	CAAATTG	657

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294

GGTATTAAAC	TAGGGGGTAT	TAACATGGCA	GGCACACAAG	CTATATATGA	ATCATCTTCT	60
GCAGGATTCT	TATCGCAAGT	CTCCTCAATC	ATCTCAAGCA	CAAGTGGTGT	CGCAGGGCCA	120
TTTGCAGGAA	TAGTAGCGGG	CGCTATGACA	GCAGCGATTA	TTCCTATTGT	TGTGGGATTT	180
ACTAATCCGC	AAATGACCGC	TATCATGACC	CAATACAATC	AAAGCATCGC	TGAAGCTGTA	240
AGCGTGCCCTA	TGAAAGCCGC	TAACCAACAA	TACAGCCAAT	TGTATCAAGG	TTTAAACGAT	300
CAAAGCATGG	CTGTGGGAAC	AATATCT				327

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

920

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295

TTTCAATTG	AAAGGAAACG	CATGAAATTT	TTTACAAGAA	TCAGTGACAG	CTACAAGAAA	60
GTGTAGTAA	CTTTAGGGCT	AGTGGTAACA	ACCAATCCTT	TAATGGCGGT	CACCAAGTCT	120
GCAACAGGCG	TTACTGAGAC	TAAAAGTTTG	GTTATTCAGA	TCATTCTGT	TCTAGCGATC	180
GTAGGTGGTT	GCGCTTTAGG	GGTCAAAGGC	ATAGCAGATA	TTTGGAAAT	CTCTGATGAC	240
ATCAAAGAG	GTCAGCGCAC	TGTTTTTGCT	TACGCGCAAC	CCATAGCTAT	GTTAGCGGTG	300
GCAGGTGGCA	TTATCTATTT	GAGCACTAAG	TTTGGCTTCA	ATATTGGCGA	GAGTGGAGGA	360
GCTAGC						366

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2973 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296

AGCGGTATAT	CTATAAGAG	AGGGGTGTTT	GTGGCAAGCA	AACAAGCTGA	CGAACAAAAA	60
AAGCTAGTTA	TAGAGCAAGA	GGTCAAAAAG	CGGCAGTTTC	AAAAAATAGA	AGAACTTAAA	120
GCAGACATGC	AAAAGGGTGT	CAATCCCTTT	TTTAAAGTCT	TGTTTGATGG	GGGGAATAGG	180
TTGTTTGGTT	TCCCTGAAAC	TTTTATTTAT	TCTTCTATAT	TTATATTGTT	TGTAACAATT	240
GTATTATCTG	TTATTCTTTT	TCAAGCCTAT	GAACCTGTTT	TGATTGTAGC	GATTGTTATT	300
GTGCTTGTAG	CTCTTGGATT	CAAGAAAGAT	TACAGGCTTT	ATCAAAGAAT	GGAGCGAGCG	360
ATGAAATTTA	AAAAACCTTT	TTTGTTTAAG	GGCGTGAAAA	ACAAAGCGTT	CATGAGCATT	420
TTTTCCATGA	AGCCTAGTAA	AGAAATGGCT	AATGACATCC	ACTTAAATCC	AAACAGAGAA	480
GACAGGCTTG	TGAGCGCTGC	AAACTCCTAT	CTAGCGAATA	ACTATGAATG	TTTTTTAGAT	540
GATGGGTGA	TCCTTACTAA	CAACTATTCT	CTTTTAGGCA	CAATCAAATT	GGGGGGCATT	600
GATTTTTTAA	CCACTTCCAA	AAAAGATCTC	ATAGAGTTAC	ACGCTTCTAT	TTATAGCGTT	660
TTTAGGAATT	TGTTACCCC	TGAATTCAAA	TTTTATTTTC	ACACTGTAA	AAAGAAAATC	720
GTTATTGATG	AAACCAATAG	GGATTATGGT	CTTATTTTTT	CTAATGATTT	CATGCGAGCC	780
TATAATGAGA	AGCAAAAGAG	AGAAAGTTTT	TATGATATTA	GTTTTTATCT	CACCATAGAG	840
CAAGATTAT	TAGACACTCT	CAATGAACCC	GTTATGAATA	AAAAGCATTT	TGCAGACAAT	900
AATTTTGAAG	AGTTTCAAAG	GATTATTAGA	GCCAGCTTG	AAAACCTCAA	AGATAGGATA	960

SUBSTITUTE SHEET (RULE 26)

921

GAGCTCATAG	AAGAGCTACT	GAGTAAATAC	CACCCCACTA	GATTAAAAGA	ATACACTAAA	1020
GATGGCATT	TTTACTCCAA	ACAATGCGAA	TTTTACAATT	TTCTTGTGGG	AATGAATGAA	1080
GCCCCTTTA	TTTGCAACAG	AAAAGACTTG	TATCTCAAGG	AAAAAATGCA	TGGTGGGGTG	1140
AAAGAAGTTT	ATTTTGCCAA	TAAGCATGGA	AAAATCTTAA	ATGACGATTT	GAGTGAAAAA	1200
TATTTTAGCG	CTATTGAGAT	CAGTGAATAC	GCCCTTAAAT	CACAGAGCGA	TTTGTGTTGAT	1260
AAAATCAACG	CTCTAGACAG	CGAATTTATC	TTTATGCGATG	CTTATTCGCC	TAAAACTCA	1320
CAAGTTTAA	AGGACAAACT	AGCTTTCACC	TCTAGAAGGA	TTATTATTAG	TGGAGGCTCC	1380
AAAGAGCAAG	GCATGACTTT	GGGTTGCTTG	AGCGAATTAG	TGGGTAATGG	TGATATTACG	1440
CTAGGCAGTT	ATGGTAATTC	TTTAGTGTCTG	TTTGCTGATA	GCTTTGAAAA	AATGAAACAA	1500
AGCGTTAAGG	AATGCGTCTC	TAGTCTTAAC	GCTAAAGGTT	TTTTAGCCAA	CGCAGCGACT	1560
TTCTCTATGG	AAAATTACTT	TTTTGCCAAA	CATTGCTCTT	TTATCACGCT	TCCTTTTATT	1620
TTTGATGTAA	CTTCTAACAA	TTTGCTGAT	TTCATAGCGA	TGAGAGCGAT	GAGTTTGTAT	1680
GGCAAGAAG	ACAATAACGC	TTGGGGCAAT	AGCGTGATGA	CGTTAAAAAG	CGAGATCAAT	1740
TCGCCTTTTT	ATTGAACTT	CCACATGCCC	ACTGATTTTG	GTTTCAGCTTC	AGCAGGACAC	1800
ACTTTGATAC	TTGGCTCAAC	CGGTTCAGGT	AAGACAGTGT	TTATGTCCAT	GACTCTAAAC	1860
GCTATGGGGC	AATTTGCCTA	TAATTTTCCT	GCTAATATCA	GCAAAGACAA	GCAAAAGCTC	1920
ACTATGGTTT	ATATGGATAA	AGATTATGGC	GCTTATGGGA	ATATTGTTGC	AATGGGTGGG	1980
GAGTATGTCA	AGATTGAGCT	AGGGACAGAT	ACAGGATTAA	ATCCTTTTGC	TTGGGCAGCT	2040
TGTGTGCAAA	AAACAAATGC	AACAATGGAG	CAAAAACAAA	CAGCTATTTC	TGTTGTCAAA	2100
GAGCTTGTGA	AAAACCTAGC	AACTAAAAGC	GATGAAAAAG	ATGAAAATGG	CAACAGCATC	2160
TCTTTTAGCC	TAGCAGATTC	TAATACGCTT	GCAGCGGCAG	TAACCAACCT	TATCACAGGA	2220
GATATGAACC	TAGATTATCC	TATCACTCAA	CTTATTAATG	CTTTCGGGAA	AGACCACAAT	2280
GATCCTAATG	GGCTTGTCCG	GCGATTAGCG	CCTTTTGTGA	AATCAACCAA	TGGTGAATTT	2340
CAATGGCTTT	TTGACAATAA	AGCAACAGAT	CGCTTAGATT	TTTCAAAAAC	GATTATTGGC	2400
GTTGATGGGT	CAAGTTTCTT	AGACAATAAT	GACGTTTCGC	CTTTTATTTG	TTTTTACCTT	2460
TTGCTTCGTA	TCCAAGAAGC	AATGGATGGG	CGTAGATTTG	TCTTAGATAT	TGATGAAGCG	2520
TGGAATATTT	TAGGCGATCC	AAAGGTCGCT	TATTTTGTGA	GAGACATGCT	AAAAACTGCA	2580
AGGAAAAGAA	ACGCTATTGT	TAGACTTGCG	ACTCAAAGCA	TCACTGATCT	TTTGGCTTGC	2640
CCTATTGCTG	ATACGATTAG	AGAACAATGC	CCTACAAAGA	TTTTTTTGTG	AAACGATGGG	2700
GGTAATCTTT	CTGATTACCA	AAGATTAGCC	AATGTTACAG	AAAAAGAAAT	TGAAATCATC	2760
ACTAAGGGGC	TGGATAGGAA	AATCCTCTAC	AAACAGGATG	GAAGCCCTAG	CGTTATCGCT	2820
AGTTTTAATT	TGAGAGGCAT	TCCTAAAGAA	TATTTGAAAA	TTTATCCAC	AGATACTGTA	2880
TTTGTCAAAG	AAATTGACAA	GATTATCCAA	AACCATAGTA	TCATAGATAA	ATATCAGGCC	2940
TTGAGGCCAA	TGTATCAACA	AATAAAGGAG	TAT			2973

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297

TTTTAGTAG	CATTAATGAT	ACCAAATTTA	GATATAGAAG	GAGAAACAAT	GACTAACGAA	60
GCCATTAACC	AACAACCACA	AACCGAAGCG	GCTTTTAACC	CGCAGCAATT	TATCAATAAT	120
CTTCAAGTGG	CTTTTATTAA	AGTTGATAAT	GTTGTCGCTT	CATTTGATCC	TAATCAAAAA	180
CCAATCGTTG	ATAAGAATGA	TAGGGATAAT	AGGCAAGCTT	TTGAGAAAAT	CTCGCAGCTA	240
AGGGAGGAAT	TCGCTAATAA	AGCGATCAAA	AATCCTACCA	AAAAGAATCA	GTATTTTTC	300
AGCTTTATCA	GTAAGAGCAA	TGATTTAATC	GACAAAGACA	ATCTCATTGA	TACAGGTTCT	360

SUBSTITUTE SHEET (RULE 26)

TCCATAAAGA	GCTTTTCAGAA	ATTTGGGACT	CAGCGTTACC	AAATTTTTAT	GAATTGGGTG	420
TCCCATCAAA	ACGATCCGTC	TAAAATCAAC	ACCCAAAAAA	TCCGAGGTTT	TATGGAAAAT	480
ATCATACAAC	CCCCTATCTC	TGATGATAAA	GAGAAAGCGG	AGTTTTTGAG	GTCTGCCAAA	540
CAAGCTTTTG	CAGGAATTAT	CATAGGAAAC	CAATCCGAT	CGGATCAAAA	ATTCATGGGC	600
GTGTTTGATG	AATCTTTGAA	AGAGAGGCAA	GAAGCAGAAA	AAAAATGGAGA	GCCTAATGGA	660
GATCCTACTG	GTGGGGATTG	GCTTGATATT	TTTTTATCAT	TTGTGTTTAA	CAAAAAACAA	720
TCTTCCGATC	TCAAAGAAAC	GCTCAATCAA	GAACCAAGTC	CTCATGTCCA	ACCAGATGTA	780
GCCACTACCA	CCACTGACAT	ACAAAGCTTA	CCGCCTGAAG	CTAGGGATTT	GCTTGATGAA	840
AGGGGTAAAT	TTTCTAAATT	CACTCTTGGC	GATATGAACA	TGTTAGATGT	TGAGGGAGTC	900
GCTGACATTG	ATCCTAATTA	CAAGTTCAAC	CAATTATTGA	TCCACAATAA	CGCTCTGTCT	960
TCTGTGTTAA	TGGGGAGTCA	TAATGGCATA	GAACCTGAAA	AAGTTTCATT	GTTGTATGGA	1020
AACAATGGTG	GTCCTGAAGC	TAGGCATGAT	TGGAACGCCA	CCGTTGGTTA	TAAAAACCAA	1080
CGAGGCGACA	ATGTGGCTAC	ACTCATTAAT	GTGCATATGA	AAAAATGGCAG	TGGGTTAGTC	1140
ATAGCAGGTG	GTGAGAAAGG	GATTAACAAC	CCTAGTTTTT	ATCTCTACAA	AGAAGACCAA	1200
CTCACAGGCT	CACAACGAGC	ATTGAGTCAA	GAAGAGATCC	AAAACAAAGT	GGATTTTCATG	1260
GAATTTCTTG	CACAAAATAA	TGCTAAATTA	GACAACCTGA	GCAAGAAAGA	GAAAGAAAAA	1320
TTCCAAAATG	AGATTGAAGA	TTTTCAAAAA	GACTCTAAGG	CTTATTTAGA	CGCCCTAGGG	1380
AATGATCACA	TTGCTTTTGT	TTCTAAAAAA	GACAAAAAAC	ATTTAGCTTT	AGTTGCTGAG	1440
TTTGGAATG	GGGAATTGAG	CTACACTCTC	AAAGATTATG	GGAAAAAGC	AGATAAAGCT	1500
TTAGATAGGG	AGGCCAAAAAC	CACCTCTCAA	GGTAGCCTAA	AACATGATGG	CGTGATGTTT	1560
GTTGATTATT	CTAATTTCAA	ATACACCAAC	GCCTCCAAGA	GTCTTGATAA	GGGTGTGGGT	1620
GCTACGAATG	GCGTTTCCCA	TTTAGAAGCA	GGCTTTAGCA	AGGTAGCTGT	CTTTAATTTG	1680
CCTAATTTAA	ATAATCTCGC	TATCACTAGT	GTCTGAAGGC	AGGATTTAGA	GGATAAACTA	1740
ATCGCTAAAG	GATTGTCCCC	ACAAGAAGCT	AATAAGCTTG	TCAAAGATTT	TTTGAGCAGC	1800
AACAAAGAAT	TGGTTGGAAG	AGCTTTTAAAC	TTCAATAAAG	CTGTAGCTGA	AGCTAAAAAC	1860
ACAGGCAACT	ATGACGAGGT	GAAACAAGCT	CAGAAAGATC	TTGAAAAATC	TCTAAAGAAA	1920
CGAGAGCGTT	TGGAGAAAGA	TGTAGCGAAA	AATTTGGAGA	GCAAAAGCGG	CAACAAAAAT	1980
AAAAATGGAAG	CAAAATCTCA	AGCTAACAGC	CAAAAAGATG	AGATTTTTGC	GTTGATCAAT	2040
AAAGAGGCTA	ATAGGGATGC	AAGAGCAATC	GCTTACGCTC	AGAATCTTAA	AGGCATCAAA	2100
AGGGAATTGT	CTGATAAACT	TGAAAAATATC	AACAAGGATT	TGAAAGACTT	TAGTAAATCT	2160
TTTGATGAAT	TCAAAAATGG	CAAAAATAAG	GATTTTCAGCA	AGGCAGAAGA	AACACTAAAA	2220
GCCCTTAAAG	GCTCGGTGAA	AGATTTAGGT	ATCAATCCAG	AATGGATTTC	AAAAGTTGAA	2280
AACCTTAATG	CAGCTTTGAA	TGAATTCAAA	AATGGCAAAA	ATAAGGATTT	CAGCAAGGTA	2340
ACGCAAGCAA	AAAGCGACCT	TGAAAAATCC	ATTAAAGATG	TGATCATCAA	TCAAAAGATA	2400
ACGGATAAAG	TTGATAATCT	CAATCAAGCG	GTATCAGTGG	CTAAAGCAAC	GGGTGATTTT	2460
AGTGGGGTAG	AGCAAGCGTT	AGCCGATCTC	AAAAATTTCT	CAAAGGAGCA	ATTGGCTCAA	2520
CAGGCTCAAA	AAATGGAAGA	TTTCAATACT	GGAAAAAATT	CTGCACTATA	CCAATCCGTT	2580
AAGAATGGTG	TAAACGGAAC	CCTAGTCGGT	AATGGGTTAT	CTAAAGCAGA	AGCCACAAC	2640
CTTTCTAAAA	ACTTTTCGGA	CATCAAGAAA	GAGTTGAATG	CAAAACCTGG	AAATTTCAAT	2700
AACAATAACA	ATAATGGACT	CGAAAACAGC	ACAGAACCCA	TTTATACTCA	AGTTGCTAAA	2760
AAGGTAAAG	CAAAAATTGA	CCGACTCGAT	CAAAATAGCAA	GTGGTTTGCG	TGATGTAGGG	2820
CAAGCAGCGA	GCTTCCTTTT	GAAAAGGCAT	GATAAAGTTG	ATGATCTCAG	TAAGGTAGGG	2880
CTTTCAGCTA	ACCATGAACC	CATTTACGCT	ACGATTGATG	ATCTCGGCGG	ACCTTTCCCT	2940
TTGAAAAGGC	ATGATAAAGT	TGATGATCTC	AGTAAGGTAG	GGCTTTCAAG	GGAGCAAAAA	3000
TTGACTCAGA	AAATTGACAA	TCTCAACCGA	GCGGTATCAG	AAGCTAAAGC	AAGTCATTTT	3060
GACAACCTAG	ATCAAATGAT	AGACAAGCTC	AAAGATTCTA	CAAAAAAGAA	TGTTGTGAAT	3120
CTATATGTTG	AAAGTGCAAA	AAAAGTGCTT	ACTAGTTTGT	CAGCGAAATT	GGACAATTAC	3180
GCTACTAACA	GCCACACACG	CATTAAATAGC	AATGTCAAAA	ATGGAACAAT	CAATGAAAAA	3240
GCGACCGGCA	TGCTAACGCA	AAAAAATTCT	GAGTGGCTCA	AGCTCGTGAA	TGATAAGATA	3300
GTTGCGCATA	ATGTGGGAAG	TGCTCCTTTG	TCAGCGTATG	ATAAAATTGG	ATTCAACCAA	3360
AAGAATATGA	AAGATTATTC	TGATTCGTTT	AAGTTTTCCA	CCAGGTTGAG	CAATGCCGTA	3420
AAAGACATTA	AGTCTGGCTT	TGTGCAATTT	TTAACCAATA	TATTTTCTAT	GGGATCTTAC	3480
AGCTTGATGA	AAGCAAGTGT	GGAACATGGA	GTCAAAAATA	CTAATACAAA	AGGTGGTTTT	3540
CAAAAATCT						3549

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

923

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298

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GCACTAAGTT TGGCTTCAAT ATTGGCGAGA GTGGAGGAGC TAGCTAAATT GATCAACAAT   60
AATAATAACA ATAAAAAACT GAGAGGCTTT TTTTGAAG TTCTCTTAAG TCTCGTTGTT   120
TTCAGTTCGT ATGGGTCAGC AAATGACGAT AAAGAAGCCA AAAAAGAAGC GCTAGAAAAA   180
GAAAAAACA CTCCAATGG GCTTGTTTAT ACGAATTTAG ATTTTGATAG TTTTAAAGCG   240
ACTATCAAAA ATTTGAAAGA CAAGAAAGTA ACTTTCAAAG AAGTCAATCC CGATATTATC   300
AAAGATGAAG TTTTGGACTT CGTGATTGTC AATAGAGTCC TAAAAAAAT AAAGGATTTG   360
AAGCATTACG ATCCAGTTAT TGAAAAAATC TTTGATGAAA AGGGTAAAGA AATGGGATTG   420
AATGTAGAAT TACAGATCAA TCCTGAAGTG AAAGACTTTT TACTTTCAA AAGCATCAGC   480
ACGACCAACA AACACGCTG CTTTCTATCA TTGCACGGAG AAACAAGAGA AATTTTATGC   540
GATGATAAGC TATATAATGT TTTATTGGCC GTATTCAATT CTTATGATCC TAATGATCTT   600
TTGAAACACA TTAGCACCAT AGAGTCTCTC AAAAAAATCT TTTATACGAT TACATCTGAA   660
GCGGTATATC TA                                     672

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(2) INFORMATION FOR SEQ ID NO:1299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299

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AATAATGCTA AAAATAAGAA TAAAGGAGTC AAAAGTATGA AAACGAACTT TTATAAAATT   60
AAATTACTAT TTGCTTGGTG TCTTATCATT GGCATGTTTA ACGCTCCGCT TAACGCTGAC   120
CAAAACACGG ATATAAAGA TATTAGTCCT GAAGATATGG CGCTAAATAG CGTGGGGCTT   180
GTTTCTAGAG ATCAGCTAAA AATAGAGATC CCTAAAGAAA CCCTAGAGCA AAAAGTGGCC   240
ATACTCAATG ACTATAATGA TAAGAATGTT AATATCAAGT TTGACGACAT AAGTTTAGGG   300
AGTTTCCAAC CTAATGATAA TCTAGGTATC AATGCGATGT GGGGCATTCA AAATCTTCTC   360
ATGAGCCAAA TGATGAGCAA TTACGGTCCA ACAAATCTT TCATGTATGG CTATGCGCCA   420
ACATACTCAG ATTCATCGTT TTTACCACCG ATCTTAGGGT AT                                     462

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(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1554 base pairs

SUBSTITUTE SHEET (RULE 26)

924

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300

CCTTTGTTA	AAATAAGGTT	ATTTGATTTT	ACTATAAGGT	TGTTTAAACC	TGAATTTTAC	60
ATTTTGTATT	TTTTAAAAGG	GATTAGAGTT	CTTATGATTG	AATGGATGCA	AAATCATAGA	120
AAGTATTTAG	TGGTTACGAT	ATGGATAAGC	ACGATCGCTT	TTATTGCCGC	CGGAATGATA	180
GGTTGGGGGC	AATACAGCTT	TTCTTTAGAT	AGCGATAGCG	CTGCCAAAGT	GGGACAGATT	240
AAGATTTCTC	AAGAAGAATT	AGCCCAAGAA	TACCGCCGCC	TTAAAGACGC	CTATGCTGAG	300
TCTATCCCTG	ATTTTAAAGA	ACTCACCGAA	GATCAAATCA	AAGCCATGCA	TTTAGAAAAA	360
AGCGCGCTAG	ATTCGCTCAT	CAATCAAGCT	TTATTGAGGA	ATTTTCGCTT	AGATTTAGGG	420
CTTGGTGCTA	CCAAGCAAGA	AGTGGCCAAA	GAGATCAGAA	AAACGAACGT	TTTTCAAAAA	480
GATGGCGTTT	TTGATGAAGA	ATTGTATAAA	AATATCTTAA	AACAAAGCCA	TTACCGCCCC	540
AAGCATTTTG	AAGAAAGCGT	TGAAAGGCTT	TTAATCCTTC	AAAAAATCAG	CGCTCTATT	600
CCCAAAACCA	CCACCCCTTT	GGAGCAATCC	AGTCTATCGC	TTTGGGCAAA	ATTGCAAGAC	660
AAATTAGACA	TTCTTATCCT	AAATCCTAAT	GATGTTAAAA	TCTCTCTCAA	TGAAGAAGAG	720
ATGAAAAAAT	ATTATGAAAA	CCATAGAAAG	GATTTTAAAA	AGCCCACAAG	CTTTAAACA	780
CGCTCTTTAT	ATTTTGACGC	TAGTTTAGAA	AAAACGTATT	TGAAAGAGTT	GGAGGAATAC	840
TACCATAAAA	ACAAGGTGTC	TTATTTGGAC	AAAGAGGGGA	AATTACAGGA	TTTTAAAAGC	900
GTTCAAGAGC	AAGTCAAGCA	TGATTTAAAC	ATGCAAAAGG	CGAATGAAAA	AGCCTTAAGG	960
AGCTATATCG	CTCTAAAAAA	GGGGAACGCA	CAAAACTACA	CCACGCAAGA	TTTTGAAAAA	1020
AACAACCTCC	CCTATACTGC	TGAAATCAGC	CAAAACTCA	CCGCTCTCAA	GCCCCCTGAA	1080
GTCCTAAAC	CAGAGCCTTT	TAAAGATGGT	TTTATCGTGG	TGCAGCTTGT	CTCTCAAATT	1140
AAAGACGAAT	TGCAAAATTT	TGATGAAGCC	AAAAGCGCTC	TTAAAACCCG	TCTGACTCAA	1200
GAAAAAACCC	TTATGGCGTT	GCAAACTTTA	GCTAAAGAAA	AGCTTAAGGA	TTTTAAAGGG	1260
AAAAGCGTGG	GTTATGTAAG	CCCTAATTTT	GGAGGCACTA	TCAGTGAACT	TAACCAAGAA	1320
GAGAGCGCGA	AGTTTATCAA	CACCCTTTTT	AACGCCAGG	AAAAAAAGG	GTTTGTAACC	1380
ATAGGTAATA	AAGTGGTGCT	TTATCAAATC	ACAGAGCAAA	ATTTCAATCA	CCCCTTTAGT	1440
GCAGAGAAAA	ACCAATACAT	GCAGCGTTTA	GTCAATAACA	CTAAAACGGA	TTTTTTTGAT	1500
AAAGCGTTGA	TAGAAGAATT	GAAAAACGC	TATAAGATAG	TCAAATACAT	TCAA	1554

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

925

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301

```

AAAGGTAAGC TAGGCCTATT TTACTATTTT TCAGACTTAC TAGAGTCGCT AATTTGCTTT      60
TCAAACCTCT GTTGAAGGC CTGTTGTTCG TTTCTTTTCT TTGAAAGGCG TCGTTTMTTC      120
TTGGGCTTTT TTTCCTTTTT TGAAGAAGTC TCTGGCTCTT TTGAAGCTGT TTCTTTGAGC      180
GTGTTAGCGT TAGTCATAGG GTCTAGATCT GGGTTAGAAG AATTCTGTGT CTTAGAAGAG      240
CTTATAAATT CAGGGCTATC AGTATGGCTT TCAAGCTCCC CACTGCTCCT CTTTTGGAAT      300
GCTGCCTTAG TGTCTTTC TCAGCTTGTCT TCCATTTTTT TAAGAACGAT TGCATCCACT      360
TTTCTAGCCT TTTCTTTT GCTCACCCTA ACCATGCTGA TCAAGTATTT GATATACCCA      420
TCATACATGT CCCCAAACTG CTCATGCAAA GCCCCAAAT CTGAGCCTTT G              471

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(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302

```

GGGCTTTTGA AGCCTTTAGA AGAAACCGAA ATCAAGGCGT GTAACAAAGA TATTTTACCC      60
TTAAAGCCTT ATGAAAAAGC CAAATTGATT GCTTATATCC CCCAAGTGGA ATATTATGCG      120
TTTAATTTC ACGTGTGGA TTTTGTCTTA ATGGGGAAAG CGACGCATT GAATCTGTTC      180
GCTATGCCTA AAGCTAAGCA CATTAAAGAA GCCACGAGCG TTTTAGAGCG CTTGGATTTA      240
GAGTCCTTAA AAGATCAAGG CATTACGAT TTGTCCGGCG GTCAAAGGCA GATGGTACTT      300
TTAGCCAGAA GCTTGTGGA AAGAACGCC TTATTGTTAC TGGATGAGCC TACGAGTGCG      360
TTAGATTTAA AAAACCAAGC CCTTTTTTTT GATGCGATTA AAGATGAGAT GAAAAACGA      420
GAATTGAGCG TTTTAGTCAA TATCCATGAT CCCAATTGG TTGCCAGGCA CTCCACGCAT      480
GTGGTCATGC TCAAAGATAA AAAACTTTTT TTGCAAGCTT CCACGCCAAT CGCTATGACT      540
TCACACAATT TAAGCGCGCT TTATGACACG CCCCTAGAAG CGATCTGGCA TGATGATAAG      600
CTTGTGGTGT ATGCGTTG                                     618

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(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

926

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303

AAAAAAAAAA AAAACGATGA AAAGCATATC GCTAAGCACT TTGTAGCGGT ATCCACCAAT	60
AAAGAAGCCG TGCAACAATT TGGCATTGAC GAGCATAACA TGTTTGGATT TTGGGATTTT	120
GTAGGGGGGC GTTATAGCTT GTGGTCGGCT ATTGGCTTAT CCATTATGAT CTATTTAGGG	180
AAGAAAAATT TTAACGCCCT TTTGAAAGGG GCGTATTTAA TGGATGAGCA TTTTAGAAAC	240
GCCCTTTTG AAAGCAATTT ACCCGTTTAA ATGGGATTAA TCGGCGTGTG GTATATCAAT	300
TTTTTCCAAT CCAAGGCCA CTTGATCGCC CCTTACGAC	339

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304

CACAACAAGA CACGAATGAA AAGAGCGAAA CGGAGGAAAT TTATCACTAA ATTTTCACGC	60
TACTACACCC CAAGCGTTTT ATTCATCGCC TTAATGATCG CTGTATTACC GCCCTTGTTT	120
TCTATGGGGA GCTTTGATGA GTGGATTTAT AGGGGGCTTG TGGCTTTAAT GGTGAGCTGT	180
CCTTGCGCGT TAGTGATTTC TGTGCCCTTA GGGTATTTTG GAGGCGTGGG AGCGGCGAGC	240
CGAAAGGGGA TTTTAATGAA AGGAGTGCAT GTTTTAGAGG TGCTTACCCA AACTAAAAGC	300
ATCGCCTTTG ATAAAACCGG CACTTTGACT AAAGGCGTTT TTAAAGTGGT GGATATTGTG	360
CCGCAAAACG GGCATTCTAA AGAAGAAGTT TGCATTACGC TTCTTGCTCG CAGCTTTTAT	420
CCACGCACCC GATCGCTTTA TCCATTCAAA AAGCATGCGA AGAAATGT	468

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

927

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305

CGCTCCACTC	TAGCGAGCGC	TGATGTGGGG	ATTGGCATGG	GGAAAGGATC	AGAATTGAGC	60
AAGCAAAGCG	CGGACATTGT	GATCACTAAT	GA CTCTTTAGT	CAAAGTTTAA		120
GCGATCGCTA	AAAAAACTAA	AAGCATTATT	TGGCAAAATA	TCTTGTTCCG	TTTGGGGATT	180
AAGGCGGTTT	TTATCGTGCT	AGGGCTTATG	GGGGTAGCGA	GCTTGTGGGA	AGCGGTCTTT	240
GGCGATGTGG	GGGTTACGCT	TTTAGACTTA	GCCAATTCCA	TGCGCACGAT	GAGGGCT	297

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306

CACCAATCTT	TTAAAGAGC	GTTTGAACCA	AGAAGAAAAG	GGCGAGTTTT	TAGAATAATG	60
GGTTTTGAAA	AAAGCATTTT	AGACAATTG	AACGGAGCGC	AAAAAATTGC	CGCATGCCAC	120
ATTCAAGGGC	CTTTATTGAT	TTTAGCGGGA	GCTGGGAGCG	GTAAGACTAA	GACTTTAACG	180
AGCCGTTTAG	CGTATTTGAT	TGCGCGTTGT	GGCGTGCCTA	GCGAAAACAC	TTTAACGCTC	240
ACTTTACCA	ATAAGCGAG	TAAAGAAATG	CAAGAAAGGG	CTTTGAAATT	GTTGAAAAAC	300
CAAGCCCTTA	TCCCCCCTT	GCTTTGCACT	TTCCATCGTT	TTGGTTTGCT	GTTTTTAAGG	360
CAACACATGA	ATCTTTTAAA	AAGGGCGTGC	GATTTTTTCG	TGCTAGATAG	CGATGAAGTG	420
AAAACGCTCT	GCAAACAGCT	CAAAATTTCA	AAATTCAGGG	CGAGCATTTC	TCAAATCAAA	480
AACGGCATGA	TGGATTGAG	CGTGCAAGAT	AGCGAATGTT	ACAAAGCGTA	TGAGCTTTAT	540
CAAAACGCGC	TCAAAAAAGA	CAATTTAGTG	GATTTTGACG	ATTTGCTTTG	TTTGAGCCTT	600
AAGATTTTAC	AAGATAATGA	AAAACCTCGC	AAAGAGACCA	GCGAACGCTA	CCATTACATT	660
ATGGTAGATG	AGTATCAAGA	CACGAACGCC	CTGCAACTGG	AATTTTTTAA	ACAATTGAGT	720
TTCACGCACC	ATAATTTGTG	CGTGGTGGGC	GATGACGATC	AGAGCATTTA	TGGGTTTAGG	780
GGGGCTGATA	TTTCTAACAT	TTTAAATTTT	TCCAAGCATT	TTAAAGGGGC	TAAAATAGTG	840
AAATTAGAGA	CCAACTACCG	CTCTAGCGCT	GAAATCTTAG	CGTGCGCTAA	TTCCCTGATC	900
AGCCATAACC	AACACGCCCA	CATTAAACG	CTTCAAAGTT	TCAAAGGTTT	GCACAAAAGC	960
GTGATTTGTA	AAGAATACCC	CACGCAAAAA	GAAGAGAGCC	TGGATGTGGC	TTATCAGATT	1020
CAAAGCCCTT	TTAAAGAAGG	GCGAGAAATT	AGAAAATATC	GCTATTTTGT	ATCGTTTAAA	1080
TGG						1083

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double**SUBSTITUTE SHEET (RULE 26)**

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307

TTTGTGCTGA	ATGAAGAGCA	AAATTCATTA	GAAGAAAAAG	GGGGCGAAAA	CAAAAACGAA	60
AAAGAAACCC	CCCTAAAGGG	CATTCATTCT	AAAAATCCCCT	CTTTGAAGCA	GGCTTTGGAG	120
CAGACGATTA	GTAAATCAA	AAGCTCTAAA	GAGTTTTTCA	AACAGCTTCT	ACACAATAAA	180
AAAAAGCTTT	ATATCGCGCT	TGGAATATTG	CTTTCACTCA	TCGCGCTCAT	TGTGGCTTTG	240
AGTTTGTAC	TAGGGCATAA	AAAAGAAAAT	AAACAAACTT	CTTTACAAAC	TAATACCGCC	300
ACCACCAATA	ACGAAACGCC	TAACGACACC	AATAACGCAG	AAGCCGAAGG	GCAAAATAGAA	360
AATTTAGACT	TGCTGATTT	AATCGGCAAA	GACTCTTTGA	AAAGAAACGA	TGAAAGCCAA	420
GTGGATGCGA	TGATGCAAAA	AGCGAGCCTT	TTGTATGAGC	AAGGGCAAAA	AGATGAAGCC	480
TTGCATTTGT	TTGATAAGAT	CGCTTCTTTC	TCGCAAGGGA	TTGCGAGCCA	TAATCTAGGG	540
GTGATTAAAT	TCAAAGAAAA	GGATTTTAAT	GGGGCGTTGG	ATTTGTTTGA	TTCCAGTATC	600
GCTTCTAAAG	AAAACGCGAG	CGTGAGCGCG	ATTGATGCGT	TAGTTACGGC	TTATCATTTG	660
CAAGATGCGG	ATTGTATTA	TCATTATCTA	AAAATTGTAA	GAGACACTTT	GTATAAAGAT	720
TACAAAAAGT	CTTTTTATT	CTACGCTTAC	GCACTCAAAT	CCTACTACGC	TGGAGAGTAT	780
TTTGAAGCCC	TTTCGCTTTT	AATGCACCCT	AATTCCAACG	CCTTTTTTAA	GCCTAATGCG	840
CGCTTAGCGT	CTAAATTGTT	TTTGATGTTT	AAAGATGAAA	CGAACGCTTA	CAAGCAATTG	900
CAAAAAAGTG	CGAACGCCCA	AGATGAGCTT	GCTTTAGGGC	TTTTGCAGGC	CGTTTGGGGT	960
ACTTACAAGC	AGGCTTTGGA	GCAATTGCAG	CATTATTGTC	ACAACCTACC	TAAAGATTTA	1020
AACGCTTTAA	TGGCTTTTGA	ATTGGTGAGT	TTGAAATGCG	GCGATACCTT	TAAAGCGAGC	1080
GAAGCCTTAA	ATTAGCCAG	CCATACGCAA	GAAGACACGC	TATTAGCCAA	CTCTTTTAC	1140
CCCATCAAGC	CCACTATAAA	CCCTATGTTT	TTAGACAAAG	AAAGGGCCAA	AGAGCGTTTT	1200
TGGAACACGC	AATATTTTGA	AGGTAAAAGG	GATTTTATCT	ACCGCTTGCT	GTTTTATATC	1260
GCTCCTTTTA	AGGTTTTAGA	CTCTAAAGAA	ACCTTAGGCG	TGATTGAAGA	GGGGCTGTTT	1320
CTTTTAGATT	CTGACACGCA	AAAGGATTTA	GAGGGGCAAA	GCCTTGCTTT	TAAAAGGGGG	1380
CGTTTGATGG	CGATAGCGGA	TAAAAACGCG	CTCAAGGGGT	TGAAAGAATT	AGAAAAGAAG	1440
CGTCTAAAAA	AAGCCCTTTC	TTTTTTTGAT	TTGTCTTTAA	AAAATAGCCC	CAATAACGCG	1500
CTTTTGCAAT	ATAATGTGGG	CTTGATTAT	GCGCAATTGG	AAAATTACCA	CAAAGCTTAT	1560
TTCCATTTTT	TAAGGGCTTT	CCATTGGAAT	TCTGCGGATT	ATTTGAGCGC	GGTTTTTGCG	1620
GTTTTAGCCT	CGCATTTCAC	CCATGAAGAC	ACCACGGAGT	TTTTAAGAGA	AATCACCAG	1680
AATTTTTATA	GTCATGATTT	TTCTAGCCCC	ACGCAAAAAG	CTTTACTCTC	TTCGCTCATC	1740
GCTTATTTGA	ATTACCGCAC	CAATTGGGAT	ATGGACTGGC	TCAAAAACGC	CCCTAAAAAG	1800
CTCCCTTTTT	ATTACGCGCT	AGAAGCGGTG	TTCCGTAAAG	AGAGCAAGGA	TAAAAAATTG	1860
ATGGTGCAAT	CTTTTGGGAA	TTTAAAAAAA	ATGCTCCCTA	AAGATCTCAT	CTCTAATATT	1920
TTTTATGAAA	TCGTCCTGTA	TTACGATGCG	AGCATCCGCC	ACACTTTAAG	CATTTACACC	1980
CTTTTAGATT	CGCATAAAAT	CAGTTGGGAT	CAAACCATGC	AAGGGCCCAT	TTTAGGGCGT	2040
CATTTCTACA	CTTACATGGG	ATTTATGGTC	AATGATCTGG	ATCATCAAGA	AAGATTGTTA	2100
GAGCAAAAAA	TCGCCAGTTT	AGAAAGGGGC	GAAGCCCCTA	ACGATTGTTT	GGAAAATTTA	2160
GCGCTAGTGA	GTTTGTTCAT	AGGCCAGTAT	GAAAAAGCGA	GCGCGTTGTA	TCAAAACTTA	2220
ATTGATGGGC	TTAAGGATAA	CGAGGCGCGT	TTAAAAATCC	TAGCGGGTTT	AACCTATATC	2280
GCGCAAAATA	ATTACAATAA	CGCCGCTTTA	TGGCTAGAGC	TTGGGAAATT	AGACGATCCG	2340
AATAATGAAA	ATTACCGTTA	CGCTTTAGGG	TTGTTGTATC	AAAGAAAGGG	AGACTTGAAA	2400
TCAGCGCTAA	ACCATTTTTT	AGCCATTAAA	ACCTCTGATT	TTTCGTCGCC	TTATTTTGAT	2460
TTTGAAATTG	ACACCAATCT	TTTAAAGAG	CGTTTGAACC	AAGAAGAAAA	GGGCGAGTTT	2520
TTAGAA						2526

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

929

- (A) LENGTH: 1068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308

```

AAGGTTACTA CTACCATGAT AAAAGCAATC ATTGGAAAAA TCATCGGCAC TAGAAACGAT      60
CGCTGGATCA AACAAATACAA AAAAAAAGTC CTAGCCATCA ACGCCTTAGA GCCTACTTAT      120
GAAAAAATGA GCGATGTTGA GCTGCAAAAC GCTTTTGAAG AATTAAAAAA ACGAGTGCGA      180
TCCGTAGAAA AAGATTTGCA AGAAAAAACC CTTT TAGAAG TTTTACCAGA AAGCTTTGCT      240
ATCACTAGAG AAGCGAGCAA AAGGATCTTA AAGATGCGCC ATTTTGATGT GCAACTCATT      300
GGGGGCATGG TCTTAAACGA TGGCAAGATC GCTGAAATGA AAACCGGAGA GGGTAAGACT      360
TTGGTCGCTA CTTTAGCGGT GGCTTTGAAC GCTATGAAAG GCGAGAGCGT GTATGTGGTA      420
ACCGTTAATG ATTACTTAGC CCATAGGGAT TCTAAAGAAA TGGAGCCGTT GTATCAATTC      480
TTAGGTATA GCGTAGGCAC GATCACTGCG AGCGTGCGAG ATGATGATGA GCGCTTAGAA      540
ATTTATTCTA AAGACATTGT TTATGGCACT AATAATGAAT TTGGCTTTGA TTATCTAAGG      600
GATAACATGA AATATTCTTT AGAGCATAAA GTGCAAAAAT CCCATGCGTT CGCCATTGTT      660
GATGAAGTGG ATTCCATTTT AATTGATGAA GCGAGAAGCT CTTTAATCAT TTCAGGGCCT      720
GTGGATAGGC GCATGGAAAA TTACAACAAG GCTGATGAAG TCGCTAAAAG CATGCAAGTG      780
GAAGTGGATT TCACCATAGA CGAAAAAACC CGCGCGATTT TAATCACTGA AGAGGGGATT      840
AAAAAAGCCG AAAATCTCTT TGGCGTGGAT AATTATACA AAATTGAAAA CGCCGCCCTA      900
TCGCACCATT TAGACCAAGC CTTGAAAGCG AATTACCTCT TTTTATTGA TAAAGATTAT      960
ATTGTAGCCA ATAATGAAGT GGTGATTGTA GATGAATTTA CCGGCCGTTT GTCTGAGGGG     1020
AGGCCTTTA GTGAGGCTT ACACCAGGCT TTAGAGGCTA AAGAGGCG      1068

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(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309

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AAGCTTTTTT TAAACCCCT AAAAGAAACG AGCCTTGCCC TTGTGGGAGT GGCAAAAAAT      60
ATAAAGATTG TTGCCTATAA AGCGGGCCTA AAAAGGGCTT ATTTGCCAAA TAGATCCTTA      120

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SUBSTITUTE SHEET (RULE 26)

930

ATCTTTTTC	TTATCAAGCG	TTATTTGCGT	TTTGATAAAA	GCCAGCCTTT	CATTAGTATC	180
ACTGCTTTGT	TAGCCTTTTT	TGGCGTGGCG	GTTGGCGTGA	TGGTTTTAAT	TGTGGCTATG	240
GCGATCATGA	ACGGCATGAG	TAAGGAATTT	GAAAAAAGC	TTTTTGTGAT	GAACACCCC	300
TTAACGCTCT	ATACCACAAG	CCCTTATGGG	ATCAGCGAAG	AAGTGGTTCA	AGCTTTAGAA	360
AAAAAGTTCC	CTAATTTGCT	TTTAGCCCC	TATTTGCAAA	CCCAAAGTCC	GATTAAAAAGC	420
GCGCATTCCA	TGAATGGCGG	CGTGGTGTTC	GGGGTTGATT	TTTCTAAAGA	AAGGCACATC	480
AATGAAGTTT	TAAATGACGC	CTTAAAAAAC	ATTAATGAAA	ACGATCTCTT	CAAAAACCTT	540
TTTAATTGGA	TCGTGGGGAA	AAGCTTGAGA	TACAGCTTGA	ATTTAGATCT	CAATCAAAAA	600
GCCGATTGTG	TTTTACCGA	ATTAGAGCCA	ACAGGTCTCA	CGCTCTCCCC	CATCATGAAA	660
CGCTTTACTA	TCAAAGGCGA	TTTGATTCA	GGGCTAAAT	CCTATGACAT	GAGCTACATG	720
TATGCGAGCC	TTCAAGCTAT	AAGCGCGATC	AGGAGATTAC	CCTTAGGGCT	TTATGATGGG	780
GTGCACTGCT	ATTCTAAAC	GCCCATGAAG	GATATTGAAA	AATTACGCAA	CGCTTTAAAA	840
ACAATCAACC	ACCATGGCAT	AGGCATTGAA	GGGTGGTGGC	AACAAAACGG	GAATTTTTTC	900
TCGGCGATGG	AATTGGAAAA	AAGAGCGTTA	TTCAATTGTG	TCATGCTCAT	TATTTTAAATG	960
GCGTCTTTGA	ATATCATCAG	CTCGCTTTTA	ATGGTGGTGA	TGAACAGGCG	TAAAGAAATC	1020
GCCCTACTCT	TTAGCATGGG	GAGCAGTCAA	AAAGAAATCC	AAAAAACCTT	TTTTTATTTG	1080
GGTAATATCA	TTAGT					1095

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310

AGAGGCGTGA	GCATTAAAGA	AGAGAGCCAA	ACCTTAGCCG	ATATTACTTT	CCAAAATTAT	60
TTCAGGATGT	TTTCTAAACT	TTCAGGCATG	ACAGGCACGG	CTCAAACCGA	AGCCACAGAA	120
TTTTTTAGAA	TCTACAATTT	AGAAGTGGTG	TCCATCCCTA	CTAATCTAGC	GATCAAGCGA	180
AAAGATTTGA	ACGATCTGAT	CTATAAGAGT	GAAAAAGAAA	AATTTGACGC	TGTGATCCCT	240
AAAATTAAAG	AATTACACGA	TAAGGGTCAG	CCCGTTTTAG	TCGGCACGGC	TAGCATTGAA	300
AAGAGTGAAA	CCTTGACGCG	TTTACTCAAA	AAAGAGCGCA	TCCCTCACAC	CGTTTTAAAC	360
GCCAAGCAAC	ACACTAAAGA	AGCTGAAATC	ATCAAAGACG	CCGGGCTTAA	AGGGGCGGTT	420
ACGATTGCGA	CCAACATGGC	AGGCAGGGGC	GTTGATATTA	AGCTCACTGA	TGAAGTTAAA	480
GAACCTGGGG	GGCTGTATAT	CATTGGCACT	GAAAGGCATG	AGAGCCGTAG	GATTGACAAAT	540
CAATTAAGGG	GGCGAAGCGG	GCGTCAAGGC	GATCCGGGAG	TGAGTCAGTT	TTATTTGAGC	600
TTAGAAGACA	ATCTGTTACG	CATTTTTGGG	AGCGATAGGA	CTAAGGGGGT	GATGGAAAAA	660
TTAGGGCCTA	AAGACGGCGA	ACACATTGAA	TTCAAGCTCG	TTACAAGAGC	GGTGGAAAAAC	720
GCGCAAAAAA	AAGTGGAGAA	CTTGCAATTT	GACAGCCGTA	AGCATTTGTT	AGAATACGAT	780
GATGTGGCTA	ATGAGCAACG	AACAAGCGTG	TATAATCTTA	GAGATGAATT	ATTAGACATC	840
AATTACGATA	TTAGCGCTAA	AATCGCTGAA	AACAGAGAAT	ACGCGCTCAA	TCAAATCTTT	900
TCTAAACTCA	AAGCCTTTGA	CCATCAAAAC	CTGTCTGAAG	AGGAACTTTT	AGGGCTTAAA	960
AACATTTTAA	AAGAAGATTT	TAACGCTAGC	GTTGAATTAG	AAGATTTAGA	AAAAGCCTCC	1020
CCTATTGAAA	TATTTGTGGC	TGAAAAACTC	AAAAGCGGAT	TA		1062

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

931

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311

ATGCAGAAGT TTTTCTCTCG TTTTAGAAGG TGGGCGTTGC CCTTTTATTT TGTGAGCGCT	60
TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG CTAATAGCAT TAAATTAAGC	120
GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG CCGTGGATAG GGGGCGCAAT	180
ACCGATCACT TAAAAGATCT TAACGATTG CATGAAAAAA TCAAACATTT GCGCTTGATT	240
TTAGAGCCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAACT TGGGAGGTAA TAAGGATATG	300
AAAACGGTTG AAATCGGAAG C	321

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312

AAAAACCAAA TACTTCAAAT CCCACTGCTT CCACCCCCC CCAATAATGA AGAGCTTTTA	60
AAATCTATTA CAGATCTTAA AGATCGCCTT AAAAAATTAG AAGATCTTAA ATTAGAAGAC	120
TTTGAACCCC TTAGAAAACCT CTCTCATTTT ATAGTTATAG GTAATTTGTT TGGAAATCC	180
TCTAACGACA CCAAGAAAAA CCCAAAAGAC GCTTTAAAAT CCACCAATTT CCACGAGAAA	240
CACACCAAAC CGACTGAAAC CACCGAACTA GTTGAAGAAA ATAAAGCGCT AACCACAGAA	300
AAAGAAAGGC TAGAAAGAGA AAATAAAAAC CTAAGTGCAG ACAAGAAAAA CCTAACTAAA	360
GAAAAAACCG AATTACAAAA ACAAGTGAAT GAGTTAAAAA ACTCTAAGCA AGTTTTAGAA	420
AATGAAAAAG CCGATTGGCT AAGAGAAAAA GAAAATCTAA CCAAGACAG AGAAAACCTA	480
ACTAAAGAAA AAACAGAGCT GACTGAAAAA AATAAAGTGC TAACCACAGA AAAAGAAAGG	540
TTAGCCACAG AAAAAGAAAA CCTAACTAAA GAAAAAACCG AATCAGAAAA ACAAGTGAAT	600
GAGTTAAAAA ACTCTAAGCA AGTTTTAGAA AATGAAAAAG CCGATCTGAC CAACGAAAAC	660
ACCAAGCTAA AAACAGATAA AACAGATCTG ACTGAAAAAA ATCAAAGGCT AACCACAGAA	720
AAAACAGAAT TAAATAACAA GATTACTGGG TTAGCCACAG AAAAAGAAAG GTTAGCCGCA	780
GACAAAGAAA ACCTAACTAA AGAAAGCAGA CAAAGAAAAC CTAAC	825

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313

GCGCTTTCTA	ATTGTTTGAG	CTTGTCAGTT	AGGCGTTGGT	TTTCTTTCTC	TAAATTGGTG	60
CATCGTTTTT	CTAGAAACCC	ATGCGCATCT	TGCAATCGCG	CTCGCTCTTG	TTCGAGACTA	120
TCTCGCTCAT	TAGTGAGCGC	GGTAAC TTGG	TGTTTGAGCT	TGTCGTTTTC	GGTGGTTAGT	180
GCTTTATTTT	CTTTAGTCAG	CTCGGTGATT	TTATGGGTTA	GCTCGGTGTT	TTCTCTTTTT	240
AGCCTTTCTT	TTTCTGTGTG	CAATTCTCTT	TTTCTTCAG	TCAGCCGATC	TCTGGCTGCT	300
AATAAGCGTG	TGTTTTCTTT	AGCTAAATG	TCTTTTCCG	TTTTCAGTTC	TGCTTTTTCT	360
TTAGTGAGCT	TGTTATTGTT	TTGCCATAAT				390

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314

ATGGGAACGC	TCATTGAAAA	ATGGTTTGGC	TTCTCTCAAA	TCAGAGAAGA	ATTAGAAGCT	60
CGCATCAGTG	AGTTAGAAGA	CGAAAACACC	GAATTGTTAA	GAGAAAGAGA	ATACTTAGCT	120
GCAGAAACTA	GCGAGTTAAA	AGACGCTAAC	GATCAATTAC	GGCAAAAAAA	CGACAAGTTA	180
TTCATAACAA	AAGACAAGCT	AACCAAAGAA	AACACCGAGT	TATTCGCAGA	AAACGAAAGC	240
TTATCTGTAA	AAATCAGCGG	GTTAGAACAC	TCTAACGATC	AATTATGGCA	AAACAATAAC	300
AAGCTCACTA	AAGAAAAAGC	AGAACTGAAA	ACGGAAAAAG	ACATTTTAGC	TAAAGAAAAC	360
ACACGCTTAT	TAGCAGCCAG	AGATCGGCTG	ACTGAAGAAA	AAAGAGAATT	GACACAGAA	420
AAAGAAAGGC	TAAAAAGAGA	AAACACCGAG	CTAACCCATA	AAATCACCGA	GCTGACTAAA	480

SUBSTITUTE SHEET (RULE 26)

933

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GAAAATAAAG CACTAACCAC CGAAAACGAC AAGCTCAACC ACCAAGTTAC CGCGCTCAC 540
AATGAGCGAG ATAGTCTCGA ACAAGAGCGA GCGCGATTGC AAGATGCGCA TGGGTTTCTA 600
GAAAAACGAT GCACCAATTT AGAGAAAGAA AACCAACGCC TAACTGACAA GCTCAAACAA 660
TTAGAAAGCG CTCAAAAAAG CTTGGAAGAA ACTAACAATC AATTACGGCA AGCTTTAGAA 720
AACTCTAATG TCCAATTAGC ACAAGCTAAA GAAAAAATAG CCATAGAGAA AAGCGAGCTG 780
GAGCGAGAAA TCGCACGCTT GAAGAGCTTA GAGGGTATGG AAGCCAAAAG CGATCTGGAC 840
TTACACAACA GCGGTTTAGC GAGCGCAAAC GAGGATTTAA AACGCCAAA CCGAAAATTA 900
GAAGAAGAGA ACATCGCCCT CAAAGAGAGG GTTGATGGCT TGAACGAGCA GCTCTCCAAA 960
TTGCAACCAC AAAAACCACA A

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(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315

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TTTAAACCA TTGAACGAAA CGATTTTAAA TTAACGGAT TGACAAAAT TTTACAAAAC 60
AAAGGATATA AAATGAAAAC AATTAAAAAT GGTATTATGA TCGGCACACT CGGTGCGTTG 120
TTATTGAGCG GTTGTTCTAG CTTTGATGCT CAGCGTTTCG CTTGTCTCCC TAAAGACCAT 180
TCTTCAAAAAG ACGTTTCTAC CAAAAAAGAA GCGCAATACA TTCCTAAGGG CTTTTTTGAC 240
CCTTATTCTT CTAACCTAAA CCATTGGGAT TCTACATTC

```

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316

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AGCTTAAATA AGGGTCTGGC ATTGTTTTTA GTCAAAAAA TAGGCCTGGT AATAATGATT 60

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SUBSTITUTE SHEET (RULE 26)

934

TTAGTCTGCT	TTTtagCTTG	CTCGCAAGAG	AGCTTTATCA	AAATGCAAAA	AAAAGCCCCA	120
GAGCAAGAAA	ATGACGGCTC	TAAACGCCCC	AGCTATGTGG	ATTTCGGATTA	TGAAGTCTTT	180
AGCGAAACGA	TTTTTTTACA	AAACATGGTG	TATCAGCCTA	TAGAGGAAAG	AAACGCTTTT	240
TTCCAACGTA	CTAAGATGA	AGACAATTCT	TTTAACCCTG	AAAATTCCGT	GATTTTACTG	300
AATGAGCCAA	GCGATAATAG	TGAAAAAAAC	CTACTCTCAT	ACCCAAACGA	TCCCAATAAC	360
AATGAAGACA	ACGCTAATAA	TAGTCAAAAA	AATCCGTTCC	TTTACAAGCC	CAAAAGAAAA	420
ACAAAAAAC	CAAAACTCAT	TGAATATTCC	CAACAAGATT	TCTACCCCTT	AAAAAATGGG	480
GATATTATCA	TGAGTAAAGA	AGGGGATCAA	TGGTTGATAG	AAATCCAATC	CAAAGCCTTG	540
AAGCGTTTTT	TAAAAGATCA	AAACGATAAA	GATCGCCAGA	TCCAAACTTT	CACTTTTAAT	600
GACACTAAAA	CGCAAATCGC	GCAAATTAAG	GGCAAAATTT	CTTCGTATGT	TTATACCACC	660
AATAACGGTA	GCTTGAGTTT	AAGGCCTTTT	TATGAATCGT	TTTTGTTAGA	AAAAAGAGC	720
GATAATGTTT	ATACGATAGA	GAATAAGGCT	TTAGATACTA	TGGAGATTTC	AAAGTGTCAA	780
ATGGTGTTAA	AAAAGCATT	AACCGATAAA	TTAGACAGCC	AGCATAAAGC	CATCAGTATT	840
GATTTGGATT	TTAAAAAAGA	GCGCTTTAAG	AGCGATACGG	AACTCTTTT	AGAATGTCTT	900
AAGGAAAGT						909

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317

GCATGGTTAA	AAAGTAGGGT	TTAATGAAA	CGCCTTGCTG	TTGCGCTTAT	TTTGGTGTG	60
GGAGTGGTGT	GGGGGAAATC	CTTGCCTAAG	TGGGCAAAAG	ATTGCTCAA	AGAGATCGCG	120
ATTGAAAAGA	CCCAAAACCA	AGATGAAAAA	ATTTAGTGT	GTGGGATGAG	CGATATATTG	180
CTTTCAGATA	TGGATTATAG	CTTGTCCTCA	GCCAGACAAA	ACGCCTTAGA	GAAAGTGATG	240
GAAGCTTTCA	AGGGGGATAG	AATAGAGATT	AAGGCTGGTG	AGCTAAAGGC	CACTTTTATT	300
GATACGGATA	AAGTTTATGT	GCTTCTAAGA	ATCACTAAGA	AGCATGTTCG	TTTAATGAAT	360
GAG						363

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318

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GGATTGATAA TGAAAAAGAT TATTCTTGCA TGCCTTGTGG CTTTGTGTTG TGCCAATTTA    60
AGCGCAGAGC CTAAGTGGTA TAGCAAGGCC TATAACAAAA CAAACGCCCA AAAAGGCTAT    120
CTTTATGGGA GTGGTTCAGC CACTTCTAAA GAGGCTTCTA AACAAAAAGC GTTAGCGGAT    180
TTAGTGGCGT CTATTAGCGT GGTGGTCAAT TCACAAATCC ACATTCAAAA AAGTCGTGTG    240
GATAATAAGT TAAATCCAG CGATTACAAA ACGATCAACT TAAAAACCGA TGACTTGGAA    300
TTGAATAATG TAGAATTGT CAATCAAGAA GCGCAAAAAG GGATCTACTA CACCAGAGTG    360
AGGATCAATC AAAACTTGTT TTTGCAGGGT TTAAGGGATA AGTATAACGC TCTTTATGGG    420
CAGTTTTCCA CCTTAATGCC TAAGGTTTGC AAAGGGGTTT TTTACAAACA ATCCAAGAGC    480
ATGGGGGATT TATTGGCTAA AGCGGCGCCT ATGGAAAGGA TTTTAAAGC GTATTCTGTC    540
CCGTTGAGTT CGTTAGAAAA TTATGAAAAA ATCTATTACC AAAACGCTTT CAAACCTAAA    600
GTGCGAATCG CTTTGTGATG TAACAGCGAC ACAGAGATTA AAAACGCTCT CATGAGTGCT    660
TAGCTAGAG TGCTAACCCC TAGCGATGAA GAAAAACTTT ATCAAATCAA AAATGAAGTT    720
TTCACGGACA GTGCTAATGG CATCACACGC ATTAGAGTGA TTATTAGCGC GAGCGATTGT    780
CAAGGCACGC CTGTATTGAA TAGGAGTCTT GAAGTGGATG AAAAGAATAA GAATTTTGCT    840
ATCAGCGCGT TGCAATCTTT ACTTTATAAA GAATTGAAAG GTTATGCCAA TAAAGAAGGA    900
CAAGGCAATA CAGGGCTA

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(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319

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CCCCAAGAG TTGTTTTTAG GGTGCGATTC TTGCTCGCTA TCCCCCAAAT TTTAGTGGGC    60
TTAAGGATTG CGGTGGTGAT GCTAGTAGCG ATGGCTGGAA TCGGGGCACT CATTGGGGCT    120
GGGGGTTTGG GGCAGGCGAT TTTTAGAGGG CTAAACACGC AAAATACCAC GATTTTAGTG    180
GCGGGCAGCT TTATTATTGC TCTTTTATAG GTTTTAGCGG ATCAATTGTG GAGCGTGTGT    240
CAGCATGAAA ACGCCTTGCA ACGCCTATTT TCTCAAACG CCACCCAAA ACAAAAAGA    300
AGAGTTTATG TTAATTTAGC GGTGTTTCTT TTTTATTGCT TAGCGAGCGC TTATGGCTC    360
ATTCTTAGAA GTGCCATAGA AGAAAAGCCC TTAGTCGTGG CGACAAAACC TAGCAGCGAG    420
CAGTATATTT TGGGCGAAAT TTTAAGCCTT TTGTTAGAAA AACACCATAT CCTATCAAG    480
CGAGCGTTTG GCATTGGTGG GGGGACGATG AATATCCATC CGGCATTGAT TAGGGGCGAT    540
TTTGATTGTG ATGTGGAATA TACCGGCACC GCTTGGGTGA ACACGCTCAA AAACCTTTG    600
ACTCAAAAAG TGGATTTTGA AACGATTAAA AAGCGTTATG AGAAGGAATT TAATCTTTG    660
TGGGTGGGAC TTTTGGGCTT TAATAACACC TATTCTTTAG CGATTTCTAA AGAAGACGCT    720
CAAAAATACG CAATTGAAAC TTTCAGCGAT TTAGCCTTTC ATAGCCCGAA TTTTGATTTT    780
GGAGCGGAGT TTGATTTTTT TGAAGAGAGG GACGCTTTTA AGGGCTTAAT CAAAGCTTAT    840
CGCTTTTCATT TTAGAAGTTT GCATGAAATG GATATTAATT TGCCTTATAA AAGTTTTGAA    900
TCCCATAGA TCAACGCTTT AGACGCTTTC ACTACAGACG CTCAAATCAA AGAGCTGGAT    960
TTAAAGGTGC TGAAGGACGA TAAAGGGTTT TTTCTAATT ATCAGGCCGG TATTGTT    1017

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SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320

GGAGCAAAA	TGAAAAAAT	TGGTTTGAGC	TTGTGTTTGG	TTTTGAGTTT	GGGTTTTTTA	60
AAAGCCCATG	AAGTGAGCGC	TGAAGAGATT	GCGGATATTT	TCTACAAACT	CAACGCCAAA	120
GAGCCTAAAA	TGAAAATCAA	CCACACGAAG	GGGTTTITGCG	CTAAAGGCGT	GTTCCCTCCCT	180
AACCCGCAAG	CAAGAGAGGA	TTTAGAGGTG	CCACTACTCA	ATGAAAAAGA	AATCCCTGCG	240
TCTGTAAGGT	ATTCTTTAGG	GGGCGTGGCG	ATGGACGATA	AAAGCAAGGT	TAGGGGAATG	300
GCGTTTAAAC	TAGAAAATCA	AAACGCTAGT	TGGACAATGG	TGATGCTCAA	TACAGAAATC	360
AATTTTGCCA	AAAACCCTGA	AGAATTCGCC	CAATTTTITG	AAATGAGACT	TCCTAAAAAT	420
GGCCAAGGTA	GA					432

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321

CATGAGTTT	TAGCTATTAA	TGAATTGATG	TTTGACGTGT	TTTTGCCAG	CAGATTGAAA	60
CAAAAAGAGC	TTTTAGAAAA	AATTGAGGTG	ATCCAAAAGT	TTTTCCCTAA	TTTTCCCAAA	120
GAAACGCTTT	TAAACAATTA	CCAAAAAGAA	AATTCGCTCT	ATAACCATAA	CCTCATTAAA	180
GTGGTGGGCT	TCATTCCCTA	TGCCACCATG	CAATCCCTTT	ATACCAAAC	CATCCAAAC	240
CAAGGCATTT	TTGTGCGCCC	TTTAGACAAG	CGCTACTACC	CTAATAACGC	TTTAGCTTCG	300
CATGTTTTAG	GTTATGTGGG	GGTGCAAGT	TTACAAGATT	TAAAAGACGA	TGAAGAGAAT	360
CAATACAGCC	AGATTGTAGG	CAAAACCGGC	ATTGAAAAAG	AATACAACAA	GTTTTTACAA	420

937

GGCAAGGTGG	GTTATAAAAT	CATACATGTC	AATGCGCTCA	ATCAAGAATT	AGCCACCTTA	480
GAGGTCGTGC	CACCACGCTC	CAATAACCAC	TCGCAATTGA	GTTTAGACAA	ACGCTTCCAA	540
AAAGAGCAC	ACAAGCTCTT	TGTAAATAAG	AGAGGGCCTA	TTTTAGTGAT	GGATGCAGAA	600
AATGGGGAAT	TGCTCGTTGC	AGGAAGTTAC	CCTGAATACA	ATTTGAACGA	TTTGTAGGC	660
GGGATCAGTC	AAGACAAATG	GCAAAAACCTC	CAAGATGATA	TTTATAACCC	TTTATTAAAC	720
CGCTTCGCTA	ATGCCCTTGT	TCCGCCGGGA	TCTGTGGTTA	AAATGGGCGT	GGGGTTAAGC	780
TTTTTAGAAA	ACCTTCATAT	CACAGAAAAC	ACCACTATCC	CCACACCGCC	TTTTATTGAA	840
GTGGGCAAGC	GCAAATTCAG	GGACTGGAAA	AAAACAGGGC	ATGGCAATTC	TAATTTGTAT	900
AAAGCCATTA	GGGAGTCCGT	GGATGTGTAT	TTTTATAAGT	TTGGGCTTGA	AATCTCTATA	960
GAAAACTCT	CTAAACCTT	AAGGGAAGTG	GGCTTTGGGG	AAAAAACGGG	CGTTGATTG	1020
CCGAATGAAT	TTGTGGGGAT	TGTGCCGGAT	AATTTGTGGA	AGCTCAAACG	CTTCAATCAA	1080
GACTGGCGCG	TTGGGGACAC	GCTCATTACT	GCTATTGGGC	AAGGCTCTTT	TTTAGCCACG	1140
CCTTTGCAGG	TGTTAGCCTA	CACAGGACTC	ATTGCGACAG	GCAAACCTGGC	AACGCCTCAT	1200
TTTGTATACC	ATAACCAACA	ACCGCTCAAA	GACCCCTGA	ATAGTTTTC	AAAAAAGAAG	1260
CTCCAAGCCT	TGCGCGTGGG	CATGTATGAA	GTGTGTAACC	ATAAGACGG	CACCGCTTAT	1320
CATTCCACAA	GAGGTTCTAA	GGTTACCTTA	GCGTGTAATA	CCGGCACCGC	GCAAGTCGTA	1380
GAAATCGCTC	AAAACATCGT	CAATCGCATG	AAAGAAAAGG	ATATGGAATA	TTTCCATCGA	1440
TCCCATGCGT	GGATTACGGC	ATTCTTGCCC	TATGAAAAC	CCAAATACGC	TATCACTATT	1500
TTAGTAGAAC	ATGGGGAGGG	AGGGTCAAAA	CTAGGGGGCT	TGTTAGTGAA	AATGAGCAAC	1560
AAACTCTATG	AGCTTGGCTA	TCTT				1584

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322

ATTAATTTTG	TTAATAAAGG	GGTTTTTATG	AACATATTCA	AGCGTATTAT	TTGCGTAACC	60
GCTATTGTTT	TAGGTTTTTT	TAACCTTTTA	GACGCCAAAC	ACCACAAAGA	AAAAAAGAA	120
GACCACAAA	TCACTCGTGA	GCTTAAAGTG	GGCGCTAACC	CTGTGCCGCA	TGCGCAAATC	180
TTGCAATCAG	TTGTGGATGA	TTTGAAAGAG	AAAGGGATCA	AATTAGTGAT	CGTGTCTTTT	240
ACGGATTATG	TGTTGCCTAA	TTTAGCGCTC	AATGACGGCT	CTTAGACGC	GAATTACTTC	300
CAGCACCGCC	CTTATTTGGA	TCCGTTTAAT	TTGGACAGAA	AAATGCACCT	TGTTGGTTTTG	360
GCCAATATCC	ATGTGGAGCC	TTTAAGATTT	TATTCTCAAA	AAATCACAGA	CATTAAAAAC	420
CTTAAAAAAG	GCTCAGTGAT	TGCTGTGCCA	AATGATCCGG	CCAATCAAGG	CAGGGCGTTG	480
ATTTTACTCC	ATAAACAAAG	CCTTATCGCT	CTCAAAGACC	CAAGCAATCT	ATACGCTACG	540
GAGTTTGATA	TTGTCAAAAA	TCCTTACAAC	ATCAAAATCA	AACCCCTAGA	AGCTGCGTTA	600
TTGCCTAAGG	TTTTAGGGGA	TGTGGATGGG	GCTATCATAA	CAGGGAATTA	TGCCTTGCAA	660
GCAAACTCA	CCGGAGCCTT	ATTTTCAGAA	GATAAGGACT	CGCCTTATGC	TAATCTTGTA	720
GCCTCTCGTG	AGGATAATGC	GCAAGATGAA	GCGATAAAG	CGTTGATTGA	AGCCTTACAG	780
AGCGAAAAGA	CCAGGAAATT	CATTTTGAT	ACCTATAAGG	GGGCGATTAT	CCCGGCTTTT	840

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs

SUBSTITUTE SHEET (RULE 26)

938

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323

ATGATGATAA	CCAAACAATC	GTATCAAAGA	TTCGCTTTAA	TGCGGGTTTT	TGTGTTTTCG	60
CTTTCCGGCGT	TTATTTTTTAA	CACCACGGAG	TTTGTCCCTG	TTGCACTTCT	GTCAGACATT	120
GCGAAAAGCT	TTGAAATGGA	GAGCGCAACA	GTGGGGCTTA	TGATCACTGC	TTATGCATGG	180
GTGGTGTCTC	TTGGCTCATT	GCCCTTGATG	CTGCTTAGCG	CTAAAAATGA	AAGGAAACGC	240
TTATTGCTTT	TTCTTTTCGC	TCPTTTTATT	TTCAGCCATA	TCCTTTCAGC	GTTAGCGTGG	300
AATTTTGGG	TGCTTCTCCT	TTCTCGTATG	GGTATCGCTT	TTGCCCACTC	TATTTTTTGG	360
TCCATCACGG	CTTCTTTAGT	CATTCTGTGTC	GCGCCAAGAA	ACAAAAACA	ACAGGCCTTA	420
GGGCTGTTAG	CGTTAGGGAG	TTCTTAGCGG	ATGATTTTAG	GGTTGCCGCT	TGGGAGGATC	480
ATTGGGCAAA	TTTGGGATTG	GCGATCCACT	TTTGGCGTGA	TTGGGGGCGT	TGCGACTCTT	540
ATAATGCTGC	TTATGTGGAA	ATTGCTCCCG	CATCTACCGA	GTAAGAACGC	CGGCACGCTC	600
GCAAGTGTCC	CTATATTAAT	GAAACGCCCG	CTTTTAGTGG	GGATTTATTT	GCTTGTGATC	660
ATGGTTATTT	CTGGGCATT	CACCACTTAT	AGCTATATTG	AGCCTTTTAT	CATTCAAATC	720
AGCCAATTTT	CTCCTGACAT	TACAACGCTA	ATGTTGTTTG	TGTTTGGGTT	AGCAGACGTG	780
GTGGGGAGTT	TTTGTTCGG	CCGTTTGTAT	GCGAAAAATT	CAAGAAAATT	TATCGCTTTT	840
GCAATGGTTT	TAGTCATTTG	CCCGCAACTC	TTGCTTTTTG	TGTTTAAAAA	CTTAGAGTGG	900
GTGATCTTTT	TGCAGATTTT	CTTGTGGGGG	ATTGGGATTA	CTTCACTCAC	CATTACGTTA	960
CAAAATGAGG	GTATTCAC					978

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324

AAGGGCATT	AAAAGAAACA	AAATCTTAAA	GAGGTGGCTT	TAGACGCTTT	CTTGCCTAAA	60
AGCATCAATT	ACTACCATTT	TAACGGCTCT	CTCACCCTC	CTCCTTGAC	AGAGGGGGTG	120
GATGGTTTG	TCATAGAAGA	ACCTTTGGAA	GTTTCTGCCA	AACAATTGGC	TGAAATCAAA	180
AAACGCATGA	AAAATTCGCC	CAACCAACGC	CCCGTCCAGC	CTGACTACAA	CACCGTGATC	240

SUBSTITUTE SHEET (RULE 26)

939

ATTAAAAGCT CGGCTGAGAC CCGC

264

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325

AGGATAATTA AAATGAAAAA AACTTTTTTTG ATCGCTTTAG CGCTTACGGC TTCTCTTATA	60
GGCGCTGAAA ACACCAAATG GGATTATAAA AATAAGAAA ATGGCCCGCA CCGCTGGGAC	120
AAATTGCACA AAGATTTTGA AGTGTGCAAA AGCGGTAAAA GCCAATCGCC CATCAACATT	180
GAGCATTACT ACCACACGCA AGATAAAGCC GATTTGCAAT TCAAATACGC CGCTTCTAAA	240
CCTAAAGCGG TCTTTTTCAC CCACCATACT TTAAAGGCTT CGTTTGAGCC GACTAACCAC	300
ATCAATTATA GAGGGCATGA CTATGTGTTG GATAATGTGC ATTTCCACGC CCCTATGGAG	360
TTTTTAATCA ATAATAAAC CAGGCCTTTG AGCGCGCATT TCGTGATAA AGACGCTAAA	420
GGCGCTTGT TGGTGTTAGC GATTGGGTTT	450

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326

ATGCCTGTTA TAAGAGTTTT AGTAATGCTT GCAACAATGA TGATGAAATT AGTAAAAACG	60
GCAAAAGAAA AGAAAGTTTT TAAGAAATGTG GGAATATCTA TAATGGGGAT TGCTTTTTGG	120
GAAGCGATAA AAGACTCGAT AAAAAAACAA ATTAAAAAAA GCGATTGGAT ATCGGGGAAT	180
GTTAAGACTG CGGATGATTA TTTAAAAACG CATCCTAACT CATGGTTTAA TTCAGCAATA	240
GGTGTAACAG CGATAACAGC CATGCTTATG AATGTGTGTT TTGCTGATGA CCAATCCAAA	300
AAAGAAGTGG CTCAAGCTCA AAAGGAAGCT GAAAACGCTA GGGATAGAGC GAACAAGACT	360

SUBSTITUTE SHEET (RULE 26)

940

GGGATAGAAC	TGGAACAAGA	AGAGCAAAAG	ACAGAACAAG	AAAAACAAA	GACAGAACAA	420
GAAAAACAAA	AGACAGAACA	AGAAAAACAA	AAGACAGAAC	AAGAAAAACA	AAAGACAGAA	480
CAAGAAAAAC	AAAAGACAAG	CAATATAGAG	ACTAACAATC	AAATAAAAGT	AGAACAAGAA	540
CAACAAAAGA	CAGAACAGGA	AAAACAAAAG	ACAAACAATA	CGCAAAAAGA	TTTGGTAAAC	600
AAAGCAGAAC	AAAATTGCCA	AGAAAATCAT	AATCAATTCT	TTATTAAAAA	ATTAGGAATT	660
AAGGCTGGCA	TTGCTATAGA	AATAGAAGCT	GAATGCAAAA	CCCCTAAACC	CACAAAAACC	720
AATCAAACCC	CTATCCAGCC	AAAACACCTC	CCAACTCCA	AACAACCCCA	TTCTCAAAGA	780
GGATCAAAAG	CGCAAGAGCT	TATCGCTTAT	TTGCAAAAAG	AGCTAGAATC	TCTGCCCTAT	840
TCACAAAAG	CTATCGCTAA	ACAAGTGGAT	TTTTATAGGC	CAAGTTCTAT	CGCTTATTTA	900
GAAGTAGATC	CTAGAGATTT	TAACGCTACA	GAAGAATGGC	AAAAAGAAAA	TTTAAAAATA	960
CGCTCTAAAG	CTCAAGCTAA	AATGCTTGAA	ATGAGGAGTT	TAAAACCAGA	CCCACAAGCC	1020
CACCTTTCAA	CCTCTCAAAG	CCTTTTGCTC	GTTCAAAAAA	TATTTGCTGA	TGTTAGTAAA	1080
GAAATAAAAG	TAGTTGCTAA	TACCGAGAAA	AAAGTAGAAA	AAGCGGGTTA	TGGTTATAGT	1140
AAAAGGATG						1149

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327

AATAAAAGGA	AGAACATTAA	AGAAGTTTAT	GCGGGCGAGA	TTTGCGCGTT	CGTGGGCTTG	60
AAAGACACGC	TGACTGGGGA	CAGCCTTTGC	GATGAAAAGA	ATGCGGTGGT	TTTAGAGAGA	120
ATGGAATTTT	CTGAGCCGGT	CATTACATC	GCTGTGGAGC	CTAAAACGAA	AGCAGACCAG	180
GAAAAAATGG	GCGTAGCGTT	AGGCAAGCTT	GCTGAAGAAG	ATCCAAGCTT	TAGGGTGATG	240
ACTCAAGAAG	AAACCGGTCA	AACCTTATT	GGTGGTATGG	GTGAATTGCA	CCTAGAAATC	300
ATCGTGGATA	GATTGAAGAG	AGAATTTAAG	GTGGAAGCTG	AAATCGGTCA	GCCGCAAGTC	360
GCCTTTAGAG	AGACTATCCG	CTCAAGCGTG	AGCAAAGAGC	ATAAATACGC	TAAGCAAAGT	420
GGTGGCCGTG	GGCAATACGG	GCATGTGTTT	ATCAAGCTTG	AGCCTAAAGA	GCCTGGCAGT	480
GGGTATGAAT	TTGTGAATGA	AATTTCTGGG	GGCGTGATCC	CTAAAGAATA	TATCCCTGCG	540
GTGGATAAGG	GTATCCAAGA	AGCGATGCAA	AATGGCGTTT	TGGCAGGCTA	TCCGGTGGTG	600
GATTTTAAAG	TTACCTTTTA	TGATGGGAGC	TACCATGATG	TGGATTCTTC	AGAAATGGCG	660
TTTAAAATCG	CTGGCTCTAT	GGCGTTTAAA	GAAGCGAGTC	GTGCGGCTAA	CCCGGTTTTA	720
CTAGAGCCCTA	TGATGAAAGT	GGAAGTGGA	GTCCCTGAAG	AATACATGGG	CGATGTGATT	780
GGCGATTTAA	ACAGAAGAAG	AGGGCAAATC	AATTCTATGG	ACGATAGATT	AGGTTTGAAA	840
ATCGTGAATG	CTTTCGTGCC	GTTAGTGGA	ATGTTTGGTT	ATTCTACGGA	TTTGCGATCA	900
GCCACTCAAG	GGCGTGGGAC	TTACTCTATG	GAGTTTGACC	ACTATGGCGA	AGTGCCTAGC	960
AATATCGCTA	AGGAAATCGT	GGAAAAACGC	AAAGGC			996

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

941

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328

TCTAAAAGGG	CGTTCGCAAG	CTCTTTAGTG	TCTTCTAAGC	TGTTTTTGAG	GGACAAAGAA	60
ACTCGTAAAA	GGGGTTTAGA	AACCGTAGGG	GGGCGGATAG	CCCCCACTAA	AAACCCCTTT	120
TCTTTCAAAA	AATATTGGGC	GTTTAAAAGA	GCGGGATTGT	TTTCAAACCTC	TAGGGTAAAA	180
AATCCTGTAG	GCGTTCTAAC	GCCTAAAGTT	TCAAAAATAA	TCTGTTGGTG	TTTGCTAAGC	240
TCATTTTTTA	ATTCTTGTTC	TTGCGCGATA	AAGTATTCTA	AATGGGCCAA	AGTCAAAGCG	300
GTGTCTAACA	GGCTTAAAGC	GGTGTA				327

(2) INFORMATION FOR SEQ ID NO:1329:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1314
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329

ATAAGGAATG	CCACCATGTT	TGGGAATAAG	CAGTTACAGC	TTCAAATCAG	TCAAAAAGAT	60
TCTGAGATTG	CGGAGTTAAA	AAAAGAAGTC	AATCTCTATC	AAAGCCTTTT	AAATTTGTGC	120
TTGCATGAGG	GTTTTGTAGG	TATTA AAAAC	AATAAAGTCG	TTTTTAAAAG	CGGGAATCTT	180
GCAAGCTTAA	ACAATTTAGA	AGAACAAAGC	GTTCAATTTA	AAGAAAACGC	AGAAAGCGTT	240
AAATTACAAG	GGGTTTCTTA	TTCTTTGAAA	AGCCAAAATA	TTGACGGCGT	GCAGTATTTT	300
TCATTGGCTA	AAAAACAGG	GGGTGTGGGG	GAATACCATA	AAAATGATTT	GTTTAAGACT	360
TTTTGCACGA	GCTTAAAAGA	GGGCTTAGAG	AACGCGCAAG	AAAGCATGCA	GTATTTCCAT	420
CAAGAAACAG	GCTTGCTCTT	GAATGCGGCT	AAAAATGGCG	AAGAGCATTG	TAATGAAGGA	480
TTAATAACCG	TTAATAAAAC	GGGTCAAGAC	ATTGAATCGC	TTTATGAAAA	GATGCAAAAC	540
GCCACTTCGT	TAGCGGACTC	CCTCAACCAA	CGGAGCAATG	AAATCACTCA	AGTCATTTCT	600
TTGATTGATG	ATATTGCAGA	GCAAACCAAT	CTCTTAGCCC	TAAACGCCGC	TATTGAGGCC	660
GCACGAGCGG	GTGAACATGG	CAGAGGGTTT	GCGGTGGTGG	CTGATGAGGT	GAGAAAGCTC	720
GCTGAAAAAA	CCCAAAAAGC	CACTAAAGAA	ATCGCTGTCT	TGGTTAAAAG	CATGCAACAA	780
GAAGCGAACG	ATATTCAAAC	CAACACCCAC	GATATTAATT	CTATGTAGG	CTCTATTAAG	840
GGTGATGTGG	AAGAGCTTAA	ATCCACCGTA	AAAAATAACA	TGATTGTCTG	GCAAGCCGCA	900
AAATACACCA	TCTACAATAT	CAATAACCGG	GTGTTTTGCG	GTCTGGCTAA	ACTCGATCAT	960
GTGGTCTTTA	AAAACAATCT	TTATGGCATG	GTCTTTGGTC	TCAATTCCTT	TGACATTACC	1020
AGCCATAAGA	GTTGCCGTTT	AGGCAATGG	TATTATGAGG	GTGCGGGTAA	AGAAAACCTT	1080

SUBSTITUTE SHEET (RULE 26)

942

GCTAACACTT	CAGGCTATAG	AGCTTTAGAA	AGCCACCATG	CGAGCGTGCA	TGCTGAAGCT	1140
AATGATTTGG	TTAAAGCCGT	TCAAGAAGAT	CACGTCACCG	ATTCAAAATA	CCTAGAACAT	1200
AAAGTGCATT	TAATGGAAGA	TAGCGCTAAG	CATGTCAAAG	AAAATATTGA	TAAGATGTTT	1260
TATGAAAAAC	AAGATGAACT	CAATAAAATC	ATTGAAAAAA	TTCAAAAAGG	CGAA	1314

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330

GAGTGGTTAA	TGCTAAAAAA	GATTTTTTAT	GGTTTTATCG	TTTTATTTTT	GATTATCGTA	60
GGGTGTTGG	CCGTTCTTGT	CGCTCAAGTT	TGGGTAAGTA	CGGATAAGGA	TATTGCTAAA	120
ATTAAAGATT	ATCGCCCCAG	TGTCGCTTCA	CAGATTTTAG	ACAGAAAAGG	GCGTTTGATC	180
GCTAATATTT	ATGATAAGGA	ATTTCGTTTT	TATGCGCGTT	TTGAAGAAAT	CCCCCCACGA	240
TTTGTGAAA	GCCTTCTAGC	GGTAGAAGAC	ACCCTCTTTT	TTGAGCATGG	GGGGATCAAT	300
TTAGACGCTG	TCATGCGCGC	TATGATTAAA	AACGCTAAAA	GTGGTCGTTA	CACTGAAGGG	360
GGTAGCACTC	TAACCAACA	ACTCGTTAAA	AACATGGTGC	TCACACGGGA	AAAAACCCTA	420
ACCAGAAAAC	TCAAAGAAGC	TATCATCTCC	ATACGCATTG	AAAAAGTCTT	AAGCAAAGAA	480
GAAATTTTAG	AGCGTTATTT	GAACCAAAC	TTTTTTGGGC	ATGGGTATTA	TGGCGTGAAA	540
ACCGCAAGTT	TAGGGTATTT	TAAAAAACCC	CTTGACAAAC	TCACGCTTAA	AGAAATCACC	600
ATGTTAGTCG	CCTTACCTAG	GGCTCCAAGT	TTTTATGACC	CTACCAAAAA	TTTAGAATTT	660
TCACTCTCTA	GGGCTAATGA	TATTTTAAGG	CGGTTGTATT	CTTTAGGCTG	GATTTCTTCT	720
AACGAGCTCA	AATCCGCTCT	CAATGAAGTG	CCAATCGTCT	ATAACCAAC	TTCCACGCAA	780
AATATCGCTC	CCTATGTCGT	GGATGAAGTG	TTGAAGCAAT	TGGATCAATT	AGACGGGTGA	840
AAAACCAAG	GCTATACCAT	AAAACTCACG	ATAGATTTGG	ATTACCAACG	CTTAGCGTTG	900
GAGTCTTTGC	GTTTTGGGCA	TCAAAAAATC	TTAGAAAAAA	TCGCTAAAGA	GAAGCCAAAA	960
ACTAACGCTT	CTAATGATAA	AGATGAAGAC	AACTTAAACG	CCCAGCATGA	TAGTTACAGA	1020
AACGAGCACC	GG					1032

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

943

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331

ATACGAACAC	CAATGGATAC	CATAAAAAGC	ATTCCCATAA	GAACTTTTAT	TTTACTCTAT	60
AAAAGCTCAC	CAAAATGTGT	TGTGTTGGCA	TCAATTACAG	TGCTATTGTG	CGGCATTCTT	120
CCATCTCTGA	ATATTCTTGT	TATGATAAAA	TTGATTGATA	TTGTGGTGAA	TCTATTACAA	180
AAGCATACGC	ATTTTGAATA	CAGCTTGCTG	TTACCAACTT	TACTACTATG	GGGAGCCTTG	240
CTGTTTTTAA	CGCATGTGTT	CTCAGGAATT	TTATCAAGCT	TGCAAACCAT	TATTGCCGAA	300
CAATTTTCTA	TAAATATCAT	CACTCAGCTT	GCTAATAAAC	TCACACAAGT	TAAAAATCTA	360
AATTTTITTTG	AGAATAAAGA	CCATACTATC	AAGCTTAACA	CTATCCATAA	CGGACTGCAC	420
ATCCGCCCCC	TAAATTATGT	CAGTAATCTT	TTTTTCAATC	TACAACGCAT	TATAGGGCTT	480
ATCAGTCTGT	TTGGGATATT	ATTTTCCATT	AGTATTTATC	TACCCTTTAT	AATGATTTTT	540
GCAACAGTGC	CTTGATTTCT	CATTTCCAAC	CATATAGCAA	AAAAACATAG	TGCTTCCATA	600
GATAAACTTC	AAGACCAAAA	AGAAAGCATG	CAAAATTACT	TATACTCTGG	ACTAGATAAC	660
CAAAAGAACA	AGGACAACCT	ATTTATTTAAC	TTTCATGCTAA	ATTTTTCACCA	TAAATTTATT	720
GAAACAAAAG	AATTGTATCT	CAATAATTTT	GTGAAAGTAG	CCCCAAAAAA	CTTAATATTT	780
ACCATATATG	CTGATGTTTT	AATCACCACCT	CTAAGTATTG	CACTATTTTT	TCTAATGGTT	840
TTTATTATCC	TTTCAAAATT	AATTGGTGTG	GGAGCAATTG	CTGGGTATAT	CCAAGCATTT	900
AGCTCTACCC	AACAACAACCT	ACAAGATTTA	TCAITTTTATG	GAAAGTGGTT	TTTTGCATATC	960
AATAAATACT	TTGAAAATTA	TTTCTGTATT	TTAGATTACA	AAATACCGAA	ACCAGAAAACA	1020
CAAATCAAAT	TAGAAGAAAA	AATCCATAGC	ATTACATTTG	AAAATATTAG	TTTCTCTTAT	1080
CCTAATTCAA	AACTTATTTT	TGAAAACCTT	AATCTCTCTT	TACACTCTAA	TAAAATTTAT	1140
GCATTAGTCG	GCAAGAATGC	TAGCGGAAAA	AGCAGCGTGA	TTAATTTATT	ATTAGGTTTT	1200
TATACCCCAA	ATTCAGGTCA	AATTATCATT	AATAACAAAT	ACCCATTACA	AGACTTGGAA	1260
CTAAATAGCT	ACCATCAACA	AATGAGTGCC	ATATTTCAAG	ATTTTCTCTT	TTATGCTGGG	1320
TATAGCATTG	ATGATAATCT	TTTTATGCAA	AACAATATCA	CTAAAGAGCA	ATTGAAGCAA	1380
AAAAGAGAAA	TACTAAAATC	TTTTGATGAG	AATTTTCAAA	ATTGTCTTAA	TGATTGCAAC	1440
AACACACTAT	TTGGAGCGCA	ATATAATGGG	GTAGATTTTT	CTTTAGGTCA	AAAGCAACGC	1500
ATAGCTACCA	TGAGAGCCTT	TTTAAAACCA	AGTAATTGCA	TTGTTTTAGA	TGAGCCAAGC	1560
AGCGCCATCG	ATCCCATTAT	GGAAAAAGAG	TTTTTAGATT	TTATTTTTAA	AAAATCGCAA	1620
TCTAAGATGG	CTTTAATTAT	TACACACCGC	ATGAATAGTG	TCAAGCAAGC	TAATGAAATT	1680
ATCGTGTTAG	ATCAAGGCAA	ACTAATAGAA	CAGGGCAACT	TTGAAACCCT	TATGAAAAAA	1740
CAGGGATTAT	TTTGCGAATT	GTTTTTGAAA	CAACAATAC			1779

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332

ACGCCCAGCA	TGATAGTTAC	AGAAACGAGC	ACCGTAAGA	TTTTAGCCTT	AGTGGGGGGG	60
ATTGATTATA	AAAAAAGCGC	TTTCAATCGC	GCCACGCAAG	CCAAACGGCA	GTTTGGGAGC	120
GCGATCAAGC	CTTTTGTTGA	TCAAATCGCT	TTTGATAATG	GCTATTCCAC	CACTTCCAAA	180

SUBSTITUTE SHEET (RULE 26)

944

ATCCCTGATA	CCGCGCGAAA	TTTTGAAAAT	GGCAATTATA	GTAAAAACAG	CGTGCAAAAC	240
CACGCATGGC	ACCTAGCAA	TTATACTCGC	AAATTTTAG	GGCTTGTAAC	CTTGCAAGAA	300
GCCTTGAGCC	ATTCGTTAA	TCTGGCTACG	ATTAATTTAG	CGATCGCTTG	G	351

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333

CAAGGAGTTA	CAACAATGGC	TTTTCAGGTC	AATACAAATA	TCAATGCGAT	GAATGCGCAT	60
GTGCAATCCG	CACTCACTCA	AAACGCACTT	AAAAC TTCAT	TGGAGCGATT	GAGTTCAGGT	120
TTAAGGATCA	ATAAAGCGGC	TGATGACGCA	TCAGGCATGA	CGGTGGCGGA	TTCTTTGCGT	180
TCGCAAGCGA	GCAGTTTGGG	TCAAGCGATT	CCCAACACGA	ATGACGGCAT	GGGGATTATC	240
CAGGTTGCGG	ATAAGGCTAT	GGATGAGCAA	TTAAAAATCT	TAGACACCGT	TAAGGTTAAA	300
GCGACTCAAG	CGGCTCAAGA	TGGGCAAACT	ACGGAATCTC	GTAAAGCGAT	TCAATCTGAC	360
ATCGTTCGTT	TGATCAAGG	TTTGATAAT	ATCGGTAACA	CAACGACTTA	TAACGGGCCA	420
AGCGTTATTG	TCTGGTCAAT	TCAC				444

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334

TTCAAGGTTT	GGATAATATC	GGTAACACAA	CGACTTATAA	CGGGCCAAGC	GTTATTGTCT	60
GGTCAATTCA	CTAACAAAGA	ATTCCAAGTA	GGGGCTTATT	CTAACCAAAG	CATTAAAGGCT	120
TCTATCGGCT	CTACCACTTC	CGATAAAATC	GGTCAGGTTT	GTATCGCTAC	AGGCGCGTTA	180
ATCACGGCTT	CTGGGGATAT	TAGCTTGACT	TTTAAACAAG	TGGATGGCGT	GAATGATGTA	240

SUBSTITUTE SHEET (RULE 26)

945

ACTTTAGAGA	GCGTAAAAGT	TTCTAGTTCA	GCAGGCACAG	GGATCGGCGT	GTTAGCAGAA	300
GTGATCAATA	AAAACCTCTAA	CCGAACAGGG	GTTAAAGCTT	ATGCGAGCGT	TATCACCACG	360
AGCGATGTGG	CGGTCCAGTC	AGGAAGTTTG	AGTAATTTAA	CCTTAAATGG	GATTCATTTG	420
GGTAATATCG	CAGATATTAA	GA AAAACGAC	TCAGACGGAA	GGTTAGTCAC	AGCGATCAAT	480
GCGGTCACCT	CAGAAACCGG	TGTGGAAGCT	TATACGGATC	AAAAAGGGCG	CTTGAATTTG	540
CGCAGTATAG	ATGGTCGTGG	GATTGAAATC	AAAATTGACA	GCGTCAGTAA	CGGGCCTAGT	600
GCTTTAACTA	AACGATGGTC	AAAGAGCGGT	CAAGATGAAA	CGAAGGGATC	TACTAACTAC	660
GGAAGGTATT	CTCGGACACG	CCTAGACGTA	AGAGCATCAA	TGTCGATTCT	GTATTTAAAT	720
CACGCTTGCT	TGCTTCAGAG	CTAT				744

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335

TCACCTCTTT	GGTTAAAAAC	ACGATTCCCA	AATATTTGGC	TCGCTAAAT	CCTTTATATG	60
GCTATCTTGC	TTTGCCGCGAT	CGCTCATCT	GTGGGGCTAA	TCTTGCGCTG	GTATGTGAGT	120
GGGCATTTCG	CTTGGAGTAA	CGCTTATGAG	TCCATGCTCT	ATATCGCATG	GGCTTCTGTT	180
ATCGCAGGGT	TTGTTTACG	ATCCAAACTC	GCGCTATCGG	CTTCTAGCTT	TTTGGCCGGT	240
ATCGCGCTCT	TTGTGGCTCA	TTTAGGCTTT	ATGGACCCTC	AAATTGGCCC	TTTAGTGCCG	300
GTGTTAAAAAT	CCTATTGGCT	CAATATCCAT	GTCTCTGTCA	TCACCGCTAG	TTATGGCTTT	360
TTGGGCTTGT	GTTTTGTGCT	AGGGATTTTA				390

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336

SUBSTITUTE SHEET (RULE 26)

946

AAAAGGCTTG	AAATGGGCTT	GTCTGTAGGC	ATTGTGGGTT	TGCCTAATGT	GGGCAAATCC	60
AGCACCTTTA	ACGCGCTCAC	CAAAACCCAA	AACGCCCAAA	GTGCGAATTA	CCCTTTTTCG	120
ACCAATGAAC	CCAATAAAGC	CATTGTGAAT	GTGCCTGACA	GGCGGCTTGA	TGCGTTGGCT	180
CAAATCGTAA	AGCCTGAACG	AATCTTGCAAT	TCTGTGGTGG	AATTTGTGGA	TATTGCCGGA	240
TTGATTAAAG	GGGCGAGCAA	GGGGGAGGGT	TTAGGCAATC	AGTTTTTAGC	CAATATCAAG	300
GAATGCGAAG	TGATCTTGCA	AGTGGTGCGC	TGTTTTGAAG	ATGACAATAT	CACGCATGTG	360
AACGATAAAA	TTGACCCCTT	AAATGATATA	GAAACCATTG	AATTGGAATT	GATTTTGGCG	420
GATATTGCCA	CTTTAGACAA	AAGGATCGAT	CGCTTGCAAA	AAGCCCTAAA	AAGCTCAAAA	480
GACGCTAAAA	ATCTTTTAGA	ATGCGCTTTG	AGTTTAAAAA	CGCATTTAGA	AGAATTGAAG	540
CCGGCGAAAA	CTTTCCCTTT	AAACACGAGC	GAGGCTTTTT	TGGAATTAGA	CAAGGAATTG	600
CGTTTTTTAT	CCCATAAAAA	AATGATCTAT	GTGCGTAATG	TGGGCGAAGA	AGATTTAAAT	660
ATTCTCAACG	AGCATGCCAA	AAAAGTTGAA	AACCATGCGA	AAGTCCAAAA	TAGCGAGTTT	720
GTCGCCTTGT	GCGCTAAATT	GGAAGAAGAA	ATGGTTTCTA	TGAGTGGAGA	TGAAGTCAAA	780
GAATTTTTCG	AAAGTTTGGG	CGTAGAAGAA	AGCGGGCTAG	AAAAAACCAT	TCGTTTGAGT	840
TTTAAGGAAT	TAGGCTTGAT	CAATTATTTT	ACCGCTGGAG	TCAAGGAAGT	GCGATCATGG	900
ACGATTAAAA	AAGTTTCTAG	TGCGCCTGTG	GCTGCTGGGG	TGATCCATAA	GGATTTTGAA	960
AAAGGCTTTA	TTAGAGCTGA	AACCATCAGT	TATGACGATT	TTATCGCTTA	TAAGGGCGAA	1020
GCCGGGGCGA	AAGAAAAGGG	AGCGTTACGC	ATTGAAGGTA	AGGATTATAT	CGTTCAAGAT	1080
GGCGATGTGT	TGCATTTTCG	CTTCAATGTC				1110

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337

AGGAATAAAA	CCATGCAAGC	GTAAAAATCA	TTGCTTGAAG	TGATTACAAA	ACTCCAGAAT	60
CTAGGCGGCT	ATTTGATGCA	TATAGCTATT	TTCATCATTT	TTATTTGGAT	TGGAGGGCTT	120
AAGTTTGTGC	CTTACGAAGC	TGAAGGGATC	GCCCCTTTTC	TGGCCAACTC	CCCTTTCTTT	180
TCTTTTCATGT	ATAAATTGTA	AAAACCTGCA	TACAAACAAC	ACAAAATGTC	TGAATCCCAA	240
TCCATGCAAG	AAGAAATGCA	AGATAACCCT	AAAATCGTTG	AAAACAAAGA	ATGGCATAAA	300
GAAAACCGCA	CTTATTTAGT	GGCTGAAGGT	TTAGGGATTA	CGATCATGAT	CCTAGGCATT	360
TTGGTGCTTT	TGGGGCTTTG	GATGCCTTTA	ATGGGCGTAG	TTGGGGGCTT	CTTGTGCGTG	420
GAA						423

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338

CGATCACCAC CCTATTCTTT TTTATTCACA ACGCCAGAAG TGTTTGTCAA TCAGCATTTT	60
CCATGGCTTT CTGGGGCTGG AAGGCTAGTG GTTAAAGACT TGGCGTTATT TGCTGGAGGC	120
TTGTTGTGG CCGGATTGA TGCGAAACGC TATTGGAGG GTAAAGGGTT TTGCTTGATG	180
GACCGCTCAT CGGTAGGGAT TAAACTAAA TGCTCTAGCG GGTGTTGCTC T	231

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339

TGGTGTTTTA CAAATATTCA GGAAATCGGG AATGATTTT TAATCCCTCA AAGTTTCAAA	60
AAAAAGATT TTTCCAATTT AGCCCAACAG GTGTGCCATA GGCATGAGGG TTTTGGGGCA	120
GATGGGCTTG TGGTCGTCTT ACCGAGTAAA GATTATGACT ACGAATGGGA TTTTACAAT	180
TCAGACGGCT CTAAAGCCGG CATGTGTGGG AATGCGAGCC GTTGCCTGGG GTTATTGTC	240
TACCAACATG CTATAGCCCC TAAAGAGCAT GTTTTTTAG CCGGAAAAAG AGAGATTTCT	300
ATCCGCATAG AAGAGCCCAA CATCGTAGAG AGCAATCTCG GTAATTATCA AATCCTAGAC	360
ACCATACCCA ATTTAAGATG CAAAAAATTT TTTACTAATA ACAGCGTTT AGAAAATATC	420
CCTATGTTCT ATCTTATCAA TACAGGAGTG CCTCATTAG TGGGATTTGT GAAAAATAAA	480
GGGTATTAA ATTCTCTTAA CACACTGGAA TTAAGGGCTT TAAGGCATGA ATTTAACGCT	540
AATATTAACA TCGCTTTTAT AGAAAATAAA GAGACGATT TTTTACAAAC TTATGAGAGA	600
GGGGTTGAAG ATTTACGCT AGCTTGCGGG ACAGGCATGG CAGCGTTTT TATCGCCGCG	660
CGCCTTTTTC ATAACACCCC TAAAAAGCC ACTCTCATCC CTAAAAGCAA CGAATTTTTA	720
GAGCTTCTT TAAAAAATGA TGGAATTTT TATAAAGGAG TCGCGCGTTA TATCGGCATG	780
AGCGTTTTAG GCATGGGTGT TTTTAAAAAT GGGTGTTTT	819

(2) INFORMATION FOR SEQ ID NO:1340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1077 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

948

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1077
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340

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TTTTTGGTTC AGTTTAAATGG GGATAATTGC ATGAAAGCTC AGTATTTCCTT TTGGATTCTT      60
TTTTTGATTG GTTTTATTTC GATGCTTTAT CTGTATCAAG ATTTTTTAAT GGACGCACTG      120
ATCGCTGGGC TTTTGTGTGT GGGGCTTTTT CAAGTGAAAG TTTTITTGAA TAAACGCTTT      180
TCTAATGTTA TCAGTTCGTT TTTATGCGTT TTGGTTTTAG CGAGCGTTGT GATCGTGCCG      240
TTGTATTTTA TTGTTTATAA GGGTTCTAAT GTCATTTTTC AAATCAATTT TGAAAAACTT      300
TCAGCCTTAA TCAATATGGCT TAAAGGGACA ATCACCAGAA ATTTGTCGCA TTTTCCTGCC      360
ATTCATGATG GGGTTAGCAA GTTTTATAGAA AATTTTAGCG CCGCTTCCAT CACGGGCTAT      420
TTGTTGAAAG TGAGCAGTTA TATTGGGAAA TACAGCTTGA AACTCGTTAC AGACGCTTTA      480
TTTATCTTGG GGTTATTGTT TTTCTTTTTT TACTATGGGG AGAAATTTTA TCGTTATTTT      540
TTAGGGGTCT TGCCTCTTGA AATGAATCAA AGTAAAAAAA TTTTGAAGA AGTGGCTGGG      600
ATTTTACGAA TCGTGCCTTT AACTTCTCTC ATCAGCGTTA TTTTAGAGGG CGTGGCGTTT      660
GGGACGATGA TAATATGGTT TGGGCATGAT GGCTGGTCTT TAGGGATTTT ATACGGCCTA      720
GCGTCTTTGG TGCCGGCTGT TGGGGGGGCT TTGATTGGA TCCCTATAGC GATTTATGAG      780
CTTTATCATG GGCATGTGAA TGAGGCTATT TTTATCGTTT TGTATTCCAT TTTGTTAATT      840
GGTGTGTTGA TTGATAGCGT GATCAAGCCA ATTTTAATCG TTTTATCAA AAAAAGAATC      900
TTTAAACCAA CCTTAAAT CAATGAAATA TTGATTTTCT TTTCTATGAT TGCTGGGATT      960
TCTCAATTTG GTTTTTGGGG GATTATCGTA GGGCCTACCA TCACGCGGTT TTTTATCGCG      1020
TTACTGCGAT TGTATGAAA TTACTTTATT CAAAGGAGC AAAAAACATG CGAATGT      1077

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(2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341

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AGGTAAACA TGAATACAA AGTGCATCT GCTAGAAATA TCGCAACGCT TCTTTTCTTA      60
TTCTTTTCTC AAAGTGAAGC TTTGATTTC GGTAAATCG CTAAATCAA AGCGGTGCT      120
GAAAGTTTCT CTAAAGTCGG TTTCAATAAC AAACCTATCA AACTAATAA AGGGATTAC      180
CCTACCGAAA CCTTTATGAC GATTATGGCT TACATGCAGG TGGATTTTAC GGAGCTCTTG      240
CCCAAAGCG CTACGGCTAA CGGGCACCAT TTAGACGGGA GCCTTGGGGG TTGGGGGGGT      300
GCTGTGATTT ATGATAGCAC TAAGGATTTT ATTAACGAAG TTACAGGAAA ACCCTATGGG      360

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SUBSTITUTE SHEET (RULE 26)

949

GCTATGACGT	GGAACACGT	GGGCTATTGG	GGCGGTCTTG	TAGGGCAAAA	ACCATGGGCT	420
AGTTGCGGGT	TAGCCACAGG	GAATTTGACC	CAAGGCCAAT	ACGATAAGAT	GACTCAAGCT	480
GAAATGACGC	AGTTGTCTAA	TCAAGAAGCT	TTAGCGGCTT	CCACTTGCGC	AAAAACCTAT	540
CCCATCACA	CGAGAACTA	TGTGATTAT	AACGCTTACT	TGCGCTACAA	CTACAAAGAT	600
ATTTTGTAAA	TTAGGGGCGG	AAGGTACGAA	TCCCAGCGGA	TTATA		645

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342

ATTTTCTATC	CAAAATGGGTA	TAATAATCGC	ATGGGTTTTT	TAAAAGTTTT	AAAACATGAC	60
GCTTTAGGGC	AAGTAGGGAA	TATGTATTATA	GGGAATTTCT	TAATAACGCT	CACTGTTTTA	120
GCGGTTTGTT	TTTCTCTCA	AAGCGCTGAA	GAAACGACCA	TGCTCACCT	AAGCTACACG	180
CTCTTTTTTA	TTTTAGGGGC	GTTTTTATTA	GTCGCAATCA	GCGTGGGAGC	GATCAAAAAC	240
CTCAACGCGC	TTTTTCTTAA	AAGAGGGGTT	TTAAGCTTTT	CCTTACCCAT	TAGTTTGGAA	300
TCTTTATTGC	TCCCTAAAAT	CTTGCTCCCC	ATGGTGTTTT	TTATCTTCAG	TTTGTTCTGG	360
TTTGTTGGCG	GCGTGCGTTT	GGGCTATTAC	CTTTTAAACG	CGCAATCCAG	CGTGCTGTTT	420
ATCTTGCACA	CCGCTTTAAA	AACCTTTGCG	TTAAAACCCA	CTAAACTAT	AGGCGTTGCG	480
CTGTTTITAG	GGCTTGTTTT	AATGAAATTT	TTATTTGTTT	TGAGCGTTTT	AAACGCTACT	540
AGGATCAAAA	AAGCGCGTTT	TTTACTCGGG	GGGTGTTGT	TCATTCTGGT	GGGGGTTGTT	600
TTGGAATTGG	CTTCAATTC	GTTACTGCCC	TTAATGAGTT	CTAGTTTGAG	CATCAATGAG	660
GGGTTTATT	ATTTCTTGCA	ACAACAAGAA	TTACAAGAAA	ATAAATACTA	TCTTTTATGG	720
GGGTGGATT	TTTTAAAAAT	CCTTTTATTG	TATGGGGTGA	TCCGTTACTT	GCTCACGCAT	780
AAATTAGAAT	TGGAT					795

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

950

(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343

CACATGAAAG	GCTTATGGCT	TGTAATCTCT	TTAGTTTTTG	TTGGTTTTTT	GTGGGCTAAT	60
GAATCTTATG	TTTTTAACAA	TTCTAAGGGG	CGTTTAACAG	AAAAAAGCGT	TGCGTTTATA	120
GAGGGCGTTT	CTAAGAGCT	TTATCTTAAA	ACCGGCGTGC	GTTTTGCGAT	TGATATGACG	180
GATTTTGAAA	AAAATCCTAT	CGCTCTAGCG	AATAAAAAAG	AGCGCCAAAG	CTATCAAGAG	240
GGCTTTTAA	AGCAGCTCAA	ACCCCTTTT	GTGGTATTCT	TTTTCTACCA	TGACGCTCAA	300
AAAATAGAAT	TAGTGGCTAA	CCCTAAAGAT	TTGCTAGACA	CTGATAAAAT	CTTTTTTGAA	360
AAAATCGCTC	CCTTACTCCC	CACAAACGCT	AAAGAATACA	CGCCCCAAAG	AATTCAGCC	420
ATGCTCATTA	ACGGCTATTG	GGTCGCAGTA	GATGCTTTAG	CGGAAAAATA	TCATGTGAAT	480
ATCACGCAAA	ATTTTAGCGC	TCCTAAGGGA	GTAACTTTTG	TAAAGGTGGT	TATTTATATT	540
TTGTTATTGA	CGCTTTTGGG	CGCGTTTTTG	GGGCTTTATT	TTTTTAAAAA	ATCT	594

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344

GAGGGAAAAT	CAATGAAAGA	AAAAAACTTT	TGGCCTTTAG	GAATCATGAG	CGTGCTTATT	60
TTTGGGCTTG	GGATCGTGGT	GTTTTTAGTG	GTGTTTGCCC	TAAAAAATTC	GCCTAAAAAT	120
GATTTAGTGT	ATTTCAGGG	TCATAACGAA	GTGGATTAA	ACTTTAACGC	CATGCTTAAA	180
ACTTATGAAA	ACTTTAAATC	CAATTATCGT	TTTTCACTGG	GTTTAAAGCC	TCTTACCGAA	240
AGCCCTAAAA	CCCCCATTTT	GCCCTATTTT	TCTAAAGGCA	CGCATGGGGA	TAAAAAAATC	300
CAAGAAAACC	TTTTAAACAA	CGCTTTGATT	TTAGAAAAGT	CCAACACGCT	TTATGCACAA	360
TTGCAACCGC	TCAAACCCGC	TTTAGATTG	CCAAATATTC	AAGTGTATTT	AGCGTTCAT	420
CCCAGCCAAT	CCCAGCCCAG	ATTATTAGGA	ACGCTTGATT	GTAAAAACGC	ATGCGAACCT	480
TTAAAATTTG	ATTTGTTAGA	GGGCGATAAA	GTGGGGCGCT	ATAAGATCCT	TTTTAAATTT	540
GTTTTTAAAA	ATAAAGAAGA	ATTGATTTTG	GAGCAACTGG	CTTTTTTTAA	G	591

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345

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GCAAATCAAT TTGCGCTACA ATTTTCCTTT TCTAATTTCA AGCATGGCGA TTTTACCACA      60
AGGGATTTTA TGCTCTATTC TTTATTATAT GGCTATTTTA ATATCAATCT TTTCCAGTAT      120
TTGACCTTTA GAGCAGGGTT AGGGTTTTTC ATAGCCTTTT TTCTCACGCT TTTTTTAATG      180
CCTAAATTTCA TTCTATCGGC CAAGGCTAAA AAGGCTAACC AGCCCATTTT TAGCTTCGTG      240
CCAAGCCACC AGAATAAAAA GGATACCCCT ACGATGGGGG GCATTGTGTT TGTTTTTGCA      300
ACCATGTGTT CGAGCGTGTG GTGCGCGTCT TTGAGCAATC TTTATGTGTT GTTAGGGATA      360
ATCGTGTTAG TGGGCTTTAG TTTTGTGGGT TTTAGAGACG ATTACACTAA AATCAACCAG      420
CAAAATAACG CCGGGATGAG TCGGAAAATG AAATTGGGCA TGCTGTTTAT CCTTTCGCTT      480
ATAGTGTCTG TTTTATGAG CCTTAAGGGG TTGGACACTT TTTTATACGC GCCGTTTTTG      540
AAAAACCCCT TGTTTGAAAT GCCCACGATG TTAGCGGTTG GTTTTTGGGT GTTGTTTTTT      600
TTATCCACGA GCAATGCGGT GAATTTAACC GACGGGTTAG ACGGATTAGC GAGTGTGCCT      660
AGCATTTTCA CCCTCTTAAG CCTTCTATC TTTGTGTATG TGGCAGGGAA TCGGGAATTT      720
TCTAAATACT TGCTCTATCC TAAAGTCATA GATGTGGGGG AATTGTTTGT GATTTTCGCTA      780
GCATTAGTGG GATCGCTCTT TGGCTTTTTG TGGTATAACT GCAACCCGGC AAGCGTGTIT      840
ATGGGCGATA GCGGGAGTTT GGCAATAGGA GGGTTTATCG CTTATAACGC TATTGTTTCG      900
CATAATGAAA TCTTGCTCGT TTTAATGGGG TCTATTTTTG TAATAGAAAC TCTGTCTGTG      960
ATCTTGCAAG TAGGGAGCTA TAAACCCGT AAAAAACGCC TTTTTTTAAT GGCACCCATC     1020
CATCATCATT TTGAACAAAA GGTTGGGCA GAAAATAAGG TGATCGTGCG TTTTTGGATC     1080
ATTTCTATGC TGAGTAATTT AGTCGCTCTT TTGAGCTTGA AGGTGTGT      1128

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(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 909 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346

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GCAAGATTTA TTAATAATATT TGGCATGGGA AAATTTTCTA AATTAGGCTT TATTTTAGCC      60
ACTTTGGGTA GCTCTATCGG TTTAGGGCAT ATTGGCGCTT TTCCTTATAT GGTAGGTCAT      120
AATGGGGGGA GCGCGTTTGT GCTTTTATAC CTAGCACTAA CCTTGAGTTT AGGCATTGCT      180
ATGCTTTTAG TGGAATGCT GATTGGAAAT TTGGGTAAAA AAGACGTTGT TTCCAATTAT      240
CAAATCTTAG ATCCTAAAAG GAAAAAATAT TACCCCTTCA CTCTTTTTTT TATTTTAGGC      300
GGCCCTCTCA TTCTATCTTT TTATGCGGTG GTGTTAGGCT GGGTGCTTTA CTATCTTTTT      360
GTAGTAACCT TTGATTTGCC TAAAGATTTA GAGCAGGCTA AAATGCAATT CAGCATGCTT      420
CAAAATGGCA GTTTGATCTG GCCTGTATT GTGCTTAGCG CATGCTTGTT GCCGACAATA      480
TGGTTTGTGTT CTAGGGGGAT TGAAGAGGGG ATTGAAAAAT TAAATGTCGT GCTGATGCCC      540
TTATGTGTTT TGATTTTCAT AGGGCTTTTA ATCTATGCGA TGACTTTAGA AAGCATGCCT      600
AAAGCTTTGC GTTTTTTATT TAATTTTGAG ATTCAAAAGA TTGATTTTAA GGTGTGATG      660
GACGCTTTAG GGCAGATGTT TTTTCTTTG AGTTTAGGGG TAGGCACGAT CATTACTTAT      720

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SUBSTITUTE SHEET (RULE 26)

952

TCGGCTTTTA	CGCCTAAAAA	AGAAAACCTA	CTCAAAAGCT	CTCTGTTTAT	TGTTTACCG	780
GGTATTTTAA	TTTCTTTGAT	TGCCGGGGTG	ATGATTTTFA	CTTTGTGTT	TGAATACCAT	840
GCAGACGTGT	CTCAAGGGCC	AGGGCTTGT	TTTATTTCT	TACCTTTAAC	TTTCGCTAAA	900
ATGGGATCA						909

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347

AGGTGTGTTA	AAATGAAAT	TTCTTTATTG	GGGCATGGAA	AAACCACTCT	AGCCCTAGGG	60
CGTTTTTTTA	AAAAAAACCA	TAATGAAGTC	AAATTTTTTG	ATGATAAATT	CCCTGCATTT	120
TTTAAGGATA	GCGAGGGTTT	TCCTTGCTAC	CCTAGTAAGG	ATTTTAACCC	TAATGATTCC	180
CAACTAGAAA	TCGTCAGCCC	TGGCATTAGT	TTCACGCACC	CTTTAGTCAT	GAAAGCCAAG	240
CATTTAATGA	GCGAATACGA	TTATATTGAT	AGTTTGTGTT	ATCATTCTTT	CACGCCTACG	300
ATGATAAGTA	TTAGCGGCAC	TAACGGGAAA	ACCACCACGA	CCGAAATGCT	CACCACACTT	360
TTAGAAGATT	TTAAGGCTGT	GAGTGGGGGG	AATATCGGCA	CGCCCTTGAT	TGAATTGTTT	420
GAAAAACGAT	CGCCCTTGTG	GGTGCTAGAA	ACAAGCTCCT	TTTCTTTGCA	TTACACTAAT	480
AAGGCTTACC	CTTTAATCTA	CTTGCTCATC	AATGTGGAAG	CCGATCATTT	GACTTGGCAT	540
TGCAATTTTG	AAAATTATTT	GAACGCTAAA	CTCAAGGTTT	TAACATTGAT	GCCTAAAACT	600
TCGCTCGCTA	TCCTCCCTTT	AAAATTCAAA	GAACACCCTA	TGTTTCAAAA	CTCGCAAGCG	660
CAAAAAATCT	TTTTTGACAA	AAGCGAAGAG	GTTTTAGAGT	GTTTAAAAAT	CCCTTCTAAC	720
GCCCTTTTTT	TTAAGGGAGC	GTTTTTATTA	GACGCGGCTT	TAGCCCTTTT	AGTTTATGAG	780
CAATTTTAA	AAATAAGAA	TTTAAATGG	CAAGATTATA	GAGAAAACGC	CCTTAAAGA	840
CTGAACGCTT	TTAAAAATCGG	CTCGCATAAA	ATGGAAGAAT	TTAGGGATAA	ACAAGGGCGT	900
TTGTGGGTAG	ATGACAGCAA	AGCCACGAAT	ATTGATGCCA	CCTTACAAGC	CCTAAAAACC	960
TTTAAAAACC	AAAAAATCCA	TTTGATTTTA	GGGGGCGATA	TTAAAGGGGT	CAATTTAACC	1020
CCCCTTTTTG	AAGAGTTTAA	AAACTATAAA	ATAAGCCTTT	ATGCCATAGG	ATCAAGCGCT	1080
TCTATCATAC	AAGCCTTAGC	GTTAGAATTT	AATGTTTCTT	GTCAGGTTTG	TTTGAAGTTA	1140
GAAAAAGCGG	TTCAAGAAAT	TAAAAGCGTT	TTATTACAAA	ATGAAGTCGC	TTTGCTTTCA	1200
CCTAGCGCGG	CCAGTTTGGA	TCAATTTTCT	TCGTATAAAG	AAAGGGGTGA	AAAATTCAAA	1260
GCGTTTGT	TAAAAGAT					1278

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

953

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348

GATATGGGTA	ATCATTTTTTC	TAAATTAGGA	TTTGTTTTAG	CGGCTTTAGG	GAGCGCGATA	60
GGTTTAGGGC	ATATCTGGCG	CTTCCCCTAT	ATGACTGGGG	TGAGTGGTGG	GGGTGCTTTT	120
GTTTTATTGT	TTTTATTTTT	ATCCTTAAGC	GTGGTGCGG	CGATGTTTAT	CGCTGAAATG	180
CTATTAGGAC	AAAGCACGCA	AAAAAATGTA	ACAGAAGCTT	TTAAAGAGCT	TGACATTAAC	240
CCTAAAAAAC	GCTGGAAATA	CGCAGGGATC	ATGCTTATTT	CTGGACCTTT	AATACTGACT	300
TTTTATGGCA	CTATTTTAGG	TGGGTGCTT	TATTATTG	TGAGTATTAG	TTTTAATTTG	360
CCTAGCAGTA	TCCAAGAATC	TGAACAAATT	TTTACTCAAA	CTTTGCAGTC	TATAGGGTTA	420
CAATCCATAG	GGCTTTTAG	CGTTTTATTC	ATAACCGGAT	GGATTGTTTC	TAGGGGGATT	480
AAAGAAGGCA	TTGAAAAACT	CAATTTGGTT	TTAATGCCCT	TACTCTTTC	CACCTTTTTT	540
GGTTTGCTTT	TTTATGCGAT	GAGCATGGAT	TCTTTTTCTA	AAGCTTTCCA	TTTCATGTTT	600
GATTTCAAGC	CAAAAGATTT	GACCTCTCAA	TGTTCACTT	ATTCTTGGG	GCAGGTTTTT	660
TTTTCTCTAA	GTATCGGTTT	AGGGATCAAT	ATCACCTATG	CTGCCGTTAC	GGATAAAACG	720
CAGAATTTGC	TTAAAGCAC	GATTTGGGTG	GTTTTATCAG	GGATTTTAAT	TTCTCTTGTT	780
GGCAGGGCTT	ATGATTTTCA	CTTTTGTTT				810

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349

TGTCTCACAA	GGCACAGGGT	TAATCTTCAC	TTCTTTACCG	GTGGTTTTTG	GCCAAATGGG	60
AGCGATAGGC	GTCTTGTTT	CAATCTTTT	CTTGCTCGCG	CTCGCTTTTG	CTGGCATCAC	120
TTCTACGGTG	GCTTTATTAG	AGCCAAGCGT	GATGTATCTT	ACCGAAAAGT	ATCAATACTC	180
TCGTTT						186

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 561 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

954

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350

TTTCTCTTGT	GGGCAGGGCT	TATGATTTTC	ACTTTTGTGT	TTGAATATGG	GGCTAATGTC	60
TCACAAGGCA	CAGGGTTAAT	CTTCACTTCT	TTACCGGTGG	TTTTTGGCCA	AATGGGAGCG	120
ATAGGCGTTC	TTGTTTCAAT	TCTTTTCTTG	CTCGCGCTCG	CTTTTGCTGG	CATCACTTCT	180
ACGGTGGCTT	TATTAGAGCC	AAGCGTGATG	TATCTTACCG	AAAAGTATCA	ATACTCTCGT	240
TTTAAGGTTA	CTTGGGGTCT	TGTAGCGTTA	ATCCTTGTGG	TAGGCGTGGT	GTTGATTTTC	300
TCGCTCCATA	AGGATTATAA	AGACTATCTC	ACTTTCTTTG	AAAAAAGTCT	TTTTGATTGG	360
TTGGATTTTG	CATCAAGCAC	CATTATCATG	CCTTTAGGCG	GGATGGCAAC	CTTTATTTT	420
ATGGGCTGGG	TTTTGAAAAA	AGAAAAATTG	CGTCTTTTGA	GCGCGCACTT	TTTAGGCCCT	480
AAATTGTTTG	CAACTTGTA	TTTCTTGCTT	AAATACATCA	CCCCTTTAAT	TGTGTTTTCC	540
ATTTGGTTGA	GCAAGATTTA	T				561

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 855 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351

GAGTCTTTTA	TGGGGTGTTT	GTTTATCTTT	AAAAAAGTTA	GGGTTTATTC	TAAAATGTTG	60
GTTGCTTTGG	GGCTTTCAAG	CGTGTGTGATC	GGTTGCGCGA	TGAATCCAAG	CGCTGAGACA	120
AAAAAACCAA	ATGACGCCAA	AAACCAACAA	CCAGTTCAAA	CTCATGAAAG	AATGACAACA	180
AGTTCTGAAC	ATGTTACGCC	ACTAGATTTT	AATTACCCGG	TGCATATTGT	TCAAGCCCCA	240
CAAAACCATC	ATGTTGTAGG	TATTTTAATG	CCACGCATTC	AAGTGAGCGA	TAATCTAAAA	300
CCCTATATTG	ATAAGTTTCA	AGACGCTTTA	ATTAATCAAA	TCCAAACTAT	TTTTGAAAAA	360
AGAGGCTATC	AAGTGTGCG	TTTTCAGAT	GAAAAAGCTT	TGAATGTGCA	AGATAAGAAA	420
AAGATTTTTT	CCGTTTTGGA	TTTGAAAGGG	TGGTAGGAA	TCCTAGAAGA	TTTGAAAATG	480
AATTTAAAAG	ATCCCAATAG	TCCCAATTTA	GACACGCTAG	TGGATCAAAG	CTCAGGCTCT	540
GTATGGTTTA	ATTTTTATGA	ACCAGAAAGC	AATCGTGTCT	TCCATGATTT	TGCTGTAGAA	600
GTAGGAACCT	TTCAGGCAAT	AACATACACA	TACACCTCTA	CTAATAACGC	TTCAGGAGGG	660
TTTAATTCTT	CAAAAAGCGT	TATCCATGAA	AATTTGGATA	AGAATAGAGA	AGACGCGATA	720
CACAAGATTT	TAAACAGAAT	GTATGCGGTT	GTCATGAAAA	AAGCTGTAAC	AGAACTTACA	780
AAAGAAAAATA	TCGCCAAATA	CAGAGACGCT	ATTGATAGAA	TGAAAGGCTT	TAAAAGTTCT	840
ATGCCTCAAA	AAAAG					855

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352

GAATTGGTTT	TGTTTGAAAA	GTTGAAATTT	TTTAAATCA	AAAAAGACGA	TGAAATCAG	60
CCAGAAGTCA	ATTTAAATTC	TGAAATCTAT	GAGCAATTTA	AGGTCCTTAG	ACTCCCGCTT	120
ATTTTAATCC	AAATTGCTCGT	GCTTTTAGGC	ACTCTGGGAT	ACTTCGCCCT	AGAAAATTAT	180
AGCCTTATGC	AAGCTTTCTT	TCAAACGACT	TACACCATGA	CAGCTACAGG	GTTTGGCGCT	240
TTAAATGAAA	GCCAGTTTGG	GCCTATAAGT	ATTTTTTTAA	CTTCCATTTT	AATGTTTTGT	300
GGGACGGGAA	TTATTGCTTT	TAGCGTGGCT	ATTTAGTTA	GCGTGGTCAA	TAAAGGCACG	360
CTTACCAGAT	TGATTAAGGA	GAAAGGTATG	ATTTATAAAA	TCGCGCGCCT	TAAGGATCAT	420
TATGTGATTT	GTTACCATAA	TGAATACACC	ATTGAGTTGA	GCAAGCAGTT	TCGCTCCGCT	480
CAAATCCCCT	TTGTGGTCGT	GGATAATGAT	CCTAATTTTG	AAGAAGAAGC	CATTAAAGCAC	540
AAATACCCCT	ACTATATCAT	AGGCGATCCG	CACACCAATT	TAGCCATGCT	AAAAACCCAC	600
TTAAGCAGCG	CTAGGGGCGT	TGTGGCGTTG	TCTAAGATTT	TACCGGTGAA	CGTGGCGTTA	660
ATGGTGAGCG	TGCGCTTGTT	TGAAAAGGAA	TTAAAACGCA	AACCTTACTA	CATCATTGCG	720
AGCGCACACA	GCGATGAAGG	TTTAGAAAAA	TTAAAAAAT	TAGGGGCTGA	TATGTTGGTT	780
TCCCCTACAA	AACTCATGGC	GCAGAGAGTG	AGCGCGATGG	CGGTGCGTCC	GGATATGGAA	840
AATATCTTAG	AGCGTTTAT	CAACAAAAA	GACACGCTTT	TAGACTTAGA	GGAAGTGATT	900
GTCCCCAAAA	CCAGCTGGCT	TGTGTTAAGG	AAATTAAAAG	AAGCCCATTT	TAGAGAGATC	960
GCTAAAGCCT	TTGTGATTGG	TATCACTCAA	AAAGATGGCA	AATACATCCC	CATGCCTGAC	1020
GGGAAACGAT	TATTGCAAGC	GAATCCAAGC	TAT			1053

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353

ACCAAAAAGT TAAACAATAC TCTATTCAAT AAAGGATTAA TTATTTTAA AATGTTTAAA	60
AAAATCATTT TTTTGTGCGT TTTTGTGATA GGGGGATTG TCATTCCACC CCTTGAAGCC	120
ATGCCTATTT TCGCAATAA AACCCCAAA AAAAATTACC AAGAAGCCCA TGAAAAGCTC	180
TATAGAAGCA TCATTACCG CAAAAGCTC ACGCGTAAAA AAAGCGGGTG GTATTTTAA	240
GGGGGGGTTG GCGCTGTAGA AGCCATTAAG GACTATCAAG GCAAGGAAAT GAAAGATTGG	300
ATGCCACGCT CAATT	315

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354

ATCATGGCGT GTAAATTTTG CCCTAAGATC AGAAAAACAG ATTGGATTTT TATTTTAATC	60
GCCGCTTTAG GCTTTTATTC AGTTAATAAG CTAGGGTATG CGCCCAAATT CAATACCCCC	120
ACTCCAAAT CTTCACGCC TCCTTCACGC CCTATTGAAA AGCCTAACAA TATGACTGAA	180
GAAGAAAGGA AAAAGCGTTT TATAGAGTTG CAAAAGCAT GCTTACTTCA TAAAGACAAA	240
AAGGCATGCG AAGAGGTTTT T	261

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355

CGAGCTATCA CAACAAATCA ATTCGTAGGA ACAAACATGT TTTTAAAAC TTATCAAAA	60
TTACTGGGCG CGAGCTGTTT GGCGCTGTAT TTAGTGGGCT GTGGGAATGG TGGTGGCGGT	120

SUBSTITUTE SHEET (RULE 26)

957

GAATCGCCGG	TTGAGATGAT	TGCAAATAGC	GAGGGTACGT	TTCAAATCGA	CTCCAAAGCA	180
GATAGCATT	CTATTCAAGG	CGTGAAGCTT	AATAGAGGTA	ATTGTGCTGT	CAATTTTGTT	240
CCAGTAAGTG	AGACGTTTCA	AATGGGTGTT	TTAAGTCAAG	TTACTCCAAT	CTCTATACAG	300
GATTTTAAAG	ATATGGCAAG	CACTTATAAG	ATATTGATC	AAAAGAAAGG	GTTGGCAAAC	360
ATAGCAAATA	AAATTTCTCA	ATTAGAGCAA	AAGGGTGTGA	TGATGGAACC	TCAAACCCCTT	420
AATTTTGGAG	AAAGTTTAAA	AGGCATTTCT	CAAGGGTGCA	ATATTATAGA	GGCAGAAATA	480
CAAACCGACA	AAGGCGCTTG	GACTTTTAAC	TTTGATAAA			519

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356

ATATCAAACA	TGAAAATAC	CCCGAAAGAC	AGAGCAAGAA	TCCTTATAGA	AGAGCTTAAA	60
ATCTTGCAAG	GCGTTATCAA	CAGAAATGGCA	CAAAATTTCTT	TAGAATGCAA	AAAATGGACT	120
CTCGCTCTCG	CTGTGGGTGT	CTTATCCCTC	AAAATAGAGG	CAATTTCTAA	TTTTTATGGG	180
TTATGCGTTT	TAGGGGTGTT	GTTAGCATGT	TTTTATCTTT	TAGACGCTTA	TTATCTCATG	240
CAAGAAAGGC	TGTTTAGGGA	GCAATACCAA	TGGCTAATAA	AAAACCGACT	TAAAACCGAT	300
GAAAGGCTGT	TTGAAGTCTT	CCCTATTTCAT	CAAACCTGCC	AATCAACGCA	ATTCTTATCC	360
GCCATGCGTT	CGTTTAGTCT	TTTCCCCTAT	TGGGCGTTAG	GTTTGTGTTT	GGTGGGCTAT	420
GGTTTTTGTT	GT					432

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357

SUBSTITUTE SHEET (RULE 26)

958

CCCCTTAAAT	CAAAGGCAAG	CAAACCTTTTA	GGCGCTAACA	TCGTGTATAA	AATCCATTGT	60
TTGGTTAAAG	GGGTAACCTT	AGAGCAGCAA	AACAAGCTTT	TAAAAACCAT	TGAGCCCTTT	120
AAAAAATTCG	CTTCATTAGA	GTTTATAGAC	ATCAATTCGC	TAGATTATTC	CATAGAAAGC	180
TATCTTAATG	AGTCTTGCTC	CAAGCGTTAT	GGCGGGCTTC	TTGTTTGTG	CCGGCTCTTG	240
CTCGCTTCGC	TCTTCCCTAA	TTATTCTAAA	ATCATTTCCTA	TAGATGTGGA	TACGGTGTTC	300
TTAGGCGATG	TTGCAAGCGC	TTATTTTGCG	CTGGATAATG	AACCCACTAA	ATTGCTTGCG	360
ATGGTGAGAG	ACACTTTTTC	CCACCTTCCT	TTTGAAGCCT	TTTGTGATTT	TTGCGAACGC	420
ACATGCAAGA	ATTTTAAAT	TGATCTTTTG	CGCTTTAGCC	AAAACGAATT	AAAACGCATC	480
CATCAGGGCT	TTAACATGGG	CTTTTGGTG	GCGAATTTAG	ATTTATGGCG	CGAAAAATGGG	540
TTTGAAAAAA	TCGCTTTAGA	GTTTTTGAAA	ACTAGGGGAA	AGGATCTTTT	CTACCCTGAG	600
CAGTGTAA	TCAATATGGT	GTTTTTAGAG	CGTATTTTAG	AATTGCCTAT	TCATTATAAT	660
TGCTATTCTG	ATTTTTCFAA	AGAGCACTAC	CCTAAAAGTA	TCATCATGCT	CCATTTTCATC	720
AAATACAAGC	CGTGGCGTTC	TGTCAGTTCT	TTGAACGGGC	GTTTGATTTG	CTATGAAGCT	780
GAAGCGAGTT	TTGGCTCGC	CAACCTTTT	TGCACCCCTT	TTAAAAACGA	TTTTTTTAAA	840
GAACGCCTTG	AAATGGCTAA	AGACCAACAA	ATGCAATCTT	TTAAAACCCA	CATCCGATCA	900
AAAACGATTA	GGGATTATTT	TTATTTTAGG	ATAAAAAATA	TTTTGAAAAA	AGTTTTTCGAA	960
CTCTCT						966

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358

AAAAAGTTTT	CGAACTCTCT	TAAAGGACAA	AAAAAAACGA	TGAAATTTTT	AAAATTCCTT	60
GCCAGTAGCG	TAACTCTAGA	TGAAAAATTT	TTAATGTTCC	TTCTTTGCAA	CGCTCTTTCT	120
AACGCTTACA	AAAATAGCGA	TTTGTTTTCT	TTCTCTAAAG	GCTTTTTTAGG	CGCTTTTTTA	180
ATCGGGTTTG	TGGTGTATTA	TGGTTGCGCG	CTAATCCCTA	AAAAACGCTT	GAAATATTCA	240
TTAGAATGGC	TGTTTATAGG	AAGCGGTATT	ATTTTTAGCG	TGGCAGAAAT	TTTTACGCTG	300
TTTTATGTTT	AAATGCCTTT	TTCCAAAGGC	TTGATTGACA	CGCTTTTAGC	CACAAACAGC	360
TCTGAAACGA	TGGCGTTTAT	AAAAAGCTAT	AAAAATTATT	TGCTTTACTA	CGCTTTGATT	420
TTGATCGCTT	TGTTGATCGC	CATTAAAATC	ATTGCGTTTA	GAGCGCTTGT	GCCTGGTGTG	480
ATAGCGAGCG	TTTTAGGGCT	TTCTATCCTT	ACAATAGGGA	GCGTTCGTAA	CATTAAACAC	540
CTTACAAAGA	ACGATGCGAT	TTTAAAAAGA	TCACTCTTTT	CTCTTTCTTT	AGCTAGGGGG	600
TTTTATTCCG	CTTATTGAG	TTTGTTTGAT	CGCCAACAAG	CCATAAAAT	TTATAGCTTT	660
TTAAATAATC	TTTATTTACC	AAGCGATTAT	CTTTCTAGCA	CGGGCGATAT	TTCAAATGTC	720
GTCTTAGTCA	TCGGCGAAAG	CGCGAGCAGA	AATTTTCATG	AACTCTATGG	CTATAGCGTT	780
CCTAATAATC	CCTTATGCGA	GCGAACTCGC	CAAGCGAGAG	AGAGAGAGAG	AGAGAGTAAC	840
AACCTGTTTC	TGTTTCTGA	CACGATAAGC	AAAGAAGCCC	ACACCTCTGA	TGCTTTTGAA	900
AGCTGCTCA	ATTATAGCGA	TGCTGAAACG	ACTAAACCTT	GGTATCAATTA	CCACAACATG	960
ATAGATATTT	TCAAGCGATC	CCATTATGAA	ACTTTTTGGT	TAGAAAAACA	AATCGTCGAT	1020
GAAATGGGGG	TCACACAAAA	TCTAGTCTCT	AATCGTTCTA	AAAACCGCTA	CTATATTTTG	1080
GGAACATATG	GTGCATACGA	TGAAGAGCTA	GTGAAATTTT	ATTCTAAAAA	TGTCCAACCC	1140
CAATTAAAAA	GCAAGAATTT	TATCGTGTTT	CATTTGCTTG	GCTCTCATTC	TTGGTATGCC	1200
GATCGTTTCC	CTAAAAGCTT	TGCCAAATTC	AAACCAAGCG	ATTTGTCTTT	TTCTAATTTG	1260
CATCAAGCA	GCGATAGAGA	CAAGCAAATC	GTGCGTGATT	ATGTCAATTC	GCTTTATTAT	1320
AACGACTTTG	TTTTGAATGG	AATTTTAAAC	CTCTTTAAAG	ATAAAGACGC	TATTGTGTTT	1380

SUBSTITUTE SHEET (RULE 26)

959

TATTTGAGCG	ACCATGCGCA	AGATATTTTT	GAAAGCGGCC	CTACTTATGG	GCATAGCTGT	1440
TCTAAGCGG	GATTAGAAAT	CCCTTTTATG	ATTTATGTGA	GCGATATTTT	TAAAGAAAAA	1500
CACCCCGAGA	AAGTGAAGTT	GATTAAAAAC	GCTTTAAACA	AACCTTTCAT	GAGCGATGAT	1560
TTAATCCATT	CTCTTTTGCC	TTTGGTGCGC	ATTCACACTA	AAGATGAAAT	AGAGAGTAAA	1620
AACCTTTTTA	GCCCCCAATT	TGACGCCCAA	AGAAAAAGGG	CTGTTTGTTA	TGGCAGCATG	1680
AATTATGATA	GGAATAAA					1698

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359

AAATCTTTTA	TGCCACCCAC	ACGCCCCCAA	GCGAGTATTT	TAAGGCTAAC	CCTAAAAAAC	60
CTTTGAGCA	TGCTATCTCG	TTATTCGCTC	TGTCTGTTGA	AAAAACGCG	CTTGCAAACA	120
ACATCAAACA	GCGCACCAA	AGCATGCTTG	ATTGCGGGCT	TATTGAAGAA	ATCAAAGCCC	180
TTTATATTAA	ATACCCTAAA	GATTGCGAGC	CTTTTAAAGC	CA		222

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360

ACTTCCGCAT	CAAGGGTGGC	TAAAGACATC	ATCAGCGAGT	CTCAAACCT	TTGCGCAAGA	60
AAATTCCGCC	GTTTGATGTC	GTTATTGAAA	GAAAAAGAAA	TGCTCATTCG	CATCGGATCT	120
TATCAAATGG	GGAACGATAA	AGAGCTTGAT	GAAGCGATTA	AGAAAAAGGC	TCTAATGGAG	180
CAATTTTATG	TGCAAGATGA	AAACGCTTTA	CAGCCTTTTG	AACAAAGCTT	TCAGCAATTA	240
GAAGAAATCT	TAAGA					255

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361

GATAAAAGGA ATATCATGGA ATCACAATC ATGAACTCG CCATTGAAAC TTATAAAATC	60
ACTTTGATGA TTTCTTTACC GGTATTATTA GCGGGCTTAG TGGTGGGGCT GTTAGTCAGT	120
ATTTTTC AAG CGACCACCCA AATCAATGAA ATGACTTTGT CTTTGTGCC TAAGATTTTA	180
GCCGTGATTG GGGTGCTGAT TTTAACCATG CCGTGGATGA CGAACATGCT TTTAGATTAC	240
ACCAAAACCT TAATCAAGCT CATTCTTAAA ATCATAGGC	279

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362

AAAATGCTAG AAACCACTAT TGATTTTCT CGTTACAGCA GCGTGAAAAT CCGTGCGCCT	60
TTAAAAGTGA GCGTTT TAGA AAACGATAAT GAAATCTCTC AAGAACACCA GATCATAGGA	120
TTAGCGAACA ACCTTTTAAT CGCTCCTGAC GTGAAAAATC TCGCTTTATT AGGAAAAAAC	180
TACGATTATA TTTGCGATAA GGGTGAGTGG GTGGAGGTAG GGGGAGCGGC CAATGCGTCT	240
AAAATTTTTA ATTATTTTAG GCGCAATGAT TTAGAGGTT TAGAGTTT AGGGCAATTG	300
CCTGGCACTT TAGGGGCGTT AGTTAAATG AATGCTGGCA TGAAAGAAAT TGAAATAAAA	360
AATGTTT TGA AAAGCGCTTG CGTTAATGGC GAATGGCTAG AAAAAGAAGC TTTGGGGCTA	420
GATTATCGCA GCAGCGGTT TAATGGCGTT GTTTT GAGG CTAGGTTTAA AAAGACGCAT	480
GGTTT TAGAG AAGGGGTTT AAAAGCGTGT AAAAGCATGC GCAAAAGCCA CCCCAAATTG	540
CCTAATTTTG GGAGCTGTTT CAAAACCCG CCTAACGATT ATGCGGGGCA GGCTTTT TAGA	600

961

GGGCGTGGGC TTAAGGGGTT ATTGTCTAAA AAGAGTGGGG CTTTGCCAAA GCAACATGCG	660
AATTTTTTGG TGAATTTGGG GGGCGCAGAA TTTGAAGAAG CCCTAGATCT GATAGAAGTC	720
GCCAAAACCA GAGTGCTACA AGAATATGGC ATTCATTTAG AAGAAGAAGT GAAAATTTTA	780
AGG	783

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363

CTCAATAGCG AACATCCCTT GTTGATGCG GCTAGCAAGC AGACTTATAT CCAAATGGCG	60
AACATGATGA TGGCAGCGGC CATGTTAGGG ATTGATTCTT GCCCGATTGA AGGGTATGAT	120
CAAGAAAAAG TGGCGGCTTA TTTAGAGGAA AAAGGCTATC TAAACACGGC AGAATTTGGC	180
GTGTCGGTAA TGGCTAGTTT TGGTTATCGT AACCAAGAGA TTACCCCTAA AACCCGCTGG	240
AAGACAGAAG TTATTTATGA AGTGATTGAA	270

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364

AAAGAGATAA CCATGAGAAA ACTATTCATC CCACCTTTTAT TATTCAGCGC TTTAGAAGCG	60
AACGAGAAAA ACGGCTTTTT CATAGAAGCC GGCTTTGAAA CTGGGCTATT AGAAGGCACA	120
CAAACGCAAG AAAAAAGACA CACCACCACA AAAAACAATT ACGCAACTTA CAATTATTTA	180
CCCACAGACA CGATTTTAAA AAGAGCGGCT AATTTATTCA CCAATGCCGA AGCGATTTC	240
AAATTAAAAA TCTCATCTTT ATCCCCTGTT AGAGTGTTGT ATATGTATAA TGGTCAATTA	300
ACTATAGAAA ACTTCTTGCC TTATAATTTA AATAATGTTA AGCTTAGTTT TACAGACGCT	360

SUBSTITUTE SHEET (RULE 26)

962

CAAGGCAATG	TGATTGATCT	AGGCGTGATA	GAGACTATCC	CCAAACACTC	TAAGATTGTT	420
TTGCCCCGAG	AGGCATTTGA	TAGTCTAAAA	ATTGACCCAT	ATACTTTATT	TCTTCCAAAA	480
ATTGAAGCCA	CTAGCACTTC	TATTTCTGAC	GCTAACACGC	AGAGGGTGTT	TGAAACGCTC	540
AATAAGATT	AGACAAATTT	GGTCGTAAAT	TATAGGAATG	AAAACAAATT	TAAAGATCAC	600
GAAATCATT	GGGAAGCCTT	TACCCACAAA	ACCGCAGAAG	AATTCACCAA	TTTAATGTTG	660
AACATGATCG	CTGTTTTAGA	CTCCCAATCT	TGGGGCGATG	CGATCTTAAA	CGCTCCTTTT	720
GAGTTCACTA	ACAGCCCAAC	AGATTGCGAT	AATGATCCTT	CAAAATGCGT	AAATCCTGGG	780
ACAAACGGGC	TTGTCAATTC	TAAAGTCGAT	CAAAAATATG	TGTTAAACAA	ACAAGACATT	840
GTCAATAAAT	TTAAAAACAA	AGCGGATCTT	GATGTAATTG	TTTTAAAGGA	TTCAGGGGTT	900
GTAGGGCTTG	GGAGTGATAT	TACCCCTAGC	AACAATGATG	ATGGCAAGCA	TTATGGCCAG	960
TTAGGGGTAG	TAGCTTCTGC	TTTAGATCCT	AAAAAATCTT	TTGGCAACGA	CCTTAAGACT	1020
ATCAATTTAG	AGGATTTAAG	AACCATCTTG	CATGAATFCA	GCCACACTAA	AGGCTATGGG	1080
CATAACGGGA	ATATGACCTA	TCAAAGAGTG	CCGGTAACGA	AAGATGTCAA	G	1131

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365

ATAATGGGCG	TTGGAGAGAA	AGAAGAGAAA	AAAGAAAGCC	AAAAGGTGGC	GGTTATCACT	60
GGGGCGAGTT	CTGGGATTGG	GTTAGAGTGC	GTGTAAATGC	TGTTAAATCA	AGGCTATAAG	120
GTCTATGCGC	TCTCTAGGCA	CGCGACTTTG	TGCGTAGCGT	TAAACCATGC	GTTATGCGAG	180
TGCGTTGATA	TTGATGTGAG	CGATTCTAAC	GCTTTAAAGG	AAGTGTTTTT	AAACATCAGC	240
GCTAAAGAAG	ATCATTGCGA	CGTTTTGATC	AATTCCGCCG	GTTATGGGGT	GTTTGGGAGC	300
GTGGAAGACA	CGCCCATTTA	AGAGGTTAAA	AAGCAATTTA	GCGTGAATTT	TTTCGCCCTT	360
TGTGAAGTGG	TGCAACTTTG	TTTGCCCTTA	TTAAAAACA	AGCCTTATTC	TAAGATTTTC	420
AATCTTTCTT	CCATAGCGGG	GCGTGTGAGC	ATGCTCTTTT	TAGGCCATTA	CAGCGCGAGT	480
AAGCATGCCT	TAGAGGCTTA	TAGCGATGCC	TTGCGTTTAG	AGCTTAAGCC	CTTTAACGTT	540
CAAGTGTGTT	TGATTGAGCC	AGGCCCGGTG	AAAAGCAATT	GGGAAAAAAC	CGCTTTTGAA	600
AATGATGAGC	GGAAAGATAG	CGTTTATGCT	TTGGAAGTGA	ATGCGGCT		648

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

963

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366

GACTCAAATA	GAAGCGCTTT	TATATGCCAC	AATCTAGCGA	TGGTTTTGAT	GATTTTCACA	60
AGCATCTTGA	AGATAGCGTT	AAAAGTTTAA	TCAGAGCGAA	AAAAAATCG	TTATGGTTTT	120
CCTAGAATCT	TTGATGTTGC	AGACATAGAA	CAAGAAGAGA	GGGAAGTCAT	TGAATGGCGA	180
GAAGAAAAGA	AAGCGTCAAA	ACAAAGCTAT	AAACAAAACC	TTCAAATCAA	TAAAAATCGCT	240
AACGATTTAA	AGCGTGATAA	GATAGTGGAT	AAAAGAACGA	TTTAAAGCGT	GATAGACGCT	300
GATATAGAGC	GTGGTTTTAT	CCCGCCTAAA	GATTTGTTAA	AACAATTAGA	AAAAATTAGC	360
GCTTCTCTTT	CTAAGACAT	CGTAATAACG	ATAAAGCAAG	TAGAAAAATT	AGAGCTTAAC	420
TATGCGCTAA	TAGACAATAT	CCAACATAAC	ACGCTTGATG	ACACGCTTGA	TTTTACCTTT	480
ATTGTTGGGG	ATTCTTTGAG	CGTTCAGTCG	CTTTATGTTA	CCTTTAATCT	TGTGATTGAT	540
ATTGATAGAC	CCATGAGCGA	GCAGTTTCTC	AACCATATTG	GGAAATTGGG	GAGTTTTGAA	600
TCTAGAGAGC	AAGCGTTAGA	GTGGGTGCGA	TTATCGCAAA	CTAAACTGAT	CATTGAAACG	660
CCTAAAGAAG	CGTTAAAAAA	TGCGGAATTA	TCACAAATTG	AAGAAATATT	GACCGGCTGT	720
ATTTTAAATG	GCGCTTACCG	CCTTCAAAAC	GATCTTAAGA	AAGGGCGA		768

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367

GGCAATGCTA	GGACTTGTAT	TGTTATATGT	TGGGATTGTC	TTAATCAGCA	ATGGGATTGC	60
GGATTAACCA	AAGTCGATCC	TAAAAGCACC	GCGGTGATGA	ACTTTTTTGT	GGGCGGACTT	120
TCCATTGTTT	GTAATGTGGT	GGTCATCACT	TACTCCGCGC	TCCACCCTAC	AGCCCCGTGA	180
GAAGGTGCAG	AAGATATTGT	TCAAGTATCG	CACCATTTGA	CCAGTTTCTA	TGGGCCAGCG	240
ACTGGGTTAT	TGTTTGTTTT	TACCTACTTG	TATGCCGCTA	TCAACCACAC	TTTTGGTTTG	300
GATTGGAGAC	CCTATTCTTG	GTATAGCTTA	TTCTAGCGA	TCAACACTGT	TCCTGCTGCG	360
ATTTTATCCC	ACTATAGCGA	TATGCTTGAT	GACCACAAAG	TGTTAGGCAT	CACTGAAGGC	420
GATTGGTGGG	CAATCATATG	GTGGCTTGG	GGTGTGTTGT	GGCTTACCGC	TTTCATTGAA	480
AACATCTTGA	AAATCCCTTT	AGGGAAATTC	ACTCCATGGC	TTGCTATCAT	TGAGGGTATT	540
TTAACCGCTT	GGATCCCTGC	TTGGTTACTC	TTTATCCAAC	ACTGGGTG		588

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

964

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368

AGCATTGCCC	ATGAATATTT	AAAGGTTAAT	TTGCAAGAAA	AATTAGCCCG	TTTTAGAGAT	60
TTTGTGCATT	ATAATGAAAA	CGCCAAAGAC	TCCTTGCCTT	TAAAAGCGCT	TTTTTTAAGC	120
GGGGTGGATG	CTTTTGATTA	AGACGCGCTT	TATTATCTAG	AAAAGATCAT	GCGTTTTGGC	180
TCTAAAAATG	GGGTTTTGAG	CTTTGTCAAT	TTGGAGAGCG	AAAAAAACAA	TCAATCCGCA	240
GAAGATTTGA	AACGCTATGC	GGAGTTTTTT	AAAGACAGGA	CAAGTTTTGA	GGGGTTAAAA	300
TACCTTAATG	TAGAAATCAT	CAGCGATCAA	GGTATTAAAT	CCCAACACAT	GCAAGACTTC	360
GCTGATAAAA	TAAAAGCGTA	TTACAAGCAA	AAAAAAGAAG	TTAAAAGGGA	GTTGAAGGAC	420
TTACAAAGAG	ACAAAGAATT	TTGGACTAAA	AGCTCTCAGC	ATGAAGTAAG	CGTGCCGGTG	480
GGGTGGGATA	TTAACCATAA	GGAAGTGTGT	TTTAAAATCG	GTAACGAACA	AAACCACACG	540
CTCATTTGCG	ACCACAGCGG	GAGTGGGAAA	TCCAATTTCT	TGCATGTGTT	GATTCAAAAT	600
CTAGCTTTCT	ACTACGATCC	CGATGAAGTC	CAACTCTTTT	TGTTAGACTA	TAAAGAGGGG	660
GTGGAATTTA	ACGCGTATGT	AGCAGATCCC	GCITTAGAGC	ATGCGAGGTT	GGTGAGCGTG	720
GCGAGTTCAA	TCTCTTATGG	CATCACTTTC	TTGAAATGGC	TTTGTGATGA	AATGCAAAAA	780
AGAGCCGATC	GTTTCAAGCA	GTTTAATGTG	AAAGATTTAA	GCGATTACCG	CAAACATGAA	840
AAATGCCCCA	GACTGATCGT	GGTGATTGAT	GAATTTTCAGG	TGCTTTTTAG	CGATAATAAA	900
TCCACTAAAG	CGGTGGAGGG	GCATTTAAAC	ACCCTGCTTA	AAAAGGGCCG	TAGCTATGGG	960
GTGCATTTGG	TTTTGGCCAC	TCAAACCATG	CGCGGCACTG	ACATTAATCC	AAGCTTTAAG	1020
GCTCAAATCG	CCAACCGCAT	CGCTTTGCCT	ATGGATGCAG	AAGACAGCAG	TAGTGTTTTG	1080
GGCGATGATG	CGGCTTGTTA	GATTCAAAAC	CCAGAAGGCA	TTTTCAACAA	CAACGAGGGG	1140
AATAGAAAAA	ACCACACCAA	GATGAGTGTC	CCTAAAGCCC	CTGATGATTT	CAAATCTTTT	1200
CTCACAAAAA	TACACGCTGA	ATTTAACCAA	AGAAATCTCG	CACCCATAGA	TCGTAAAATC	1260
TATAATGGCG	AGACACCTTT	AAAAATGCCC	GACACCCTTA	AGGCTAATGA	AATGCGTTTG	1320
CATCTGGGCA	AAAAAGTGA	TTATGAGCAA	AAGGACCTGA	TAGTGGAGTT	TGAAAGTAAC	1380
GAATCGCATT	TGTTGGTGGT	GATCCAAGAT	TTAAACGCTC	GCATCGCTTT	AATGAAACTC	1440
TTATTCCAAA	ACGTTAAGAG	CGCGAACAAA	GAATTGGTTT	TTTGCATAAA	AGAAAAACGC	1500
TTGATAAGGT	CTTTTGATGC	ACAAAAAGAA	TACGGCATCA	CGCCTGTAGA	AAATATTTTA	1560
AGCGTTTTAG	ACACCGCTAT	GAATCCTAAC	AGCGCGCTTG	TGATAGACAA	TCTCAACGAA	1620
GCGAAAGAAT	TGCACGACAA	AGTAGGGGCG	GAAAAGTTAA	AATCGTTTTT	AGAAAAAGCC	1680
ATAGACAACG	AGCAGTATTG	CGTCATTTTT	GCGCATGACT	TTAGGCAAAAT	TAAAACTAAT	1740
TACCATTTTG	ACAAGTTAAA	AGAATTGTTA	AACAACCACT	TCAAGCAATG	CCTAGCCTTT	1800
AGGTGCAATG	GGGAAAACCT	GAACGCTATC	AAAAGCGATT	TGCCTCCACC	AAGCAAACCT	1860
AACGTGCTAT	TGATAGAGCT	TTCCAAAGAC	AGCGTTACTG	AATTCAGGCC	TTTCAGCTTA	1920

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

965

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369

AGGCCCCAATC TCTCTAGCCA GTTCCTTTTAC ACGGAAATGC TGAGCTTAAA ACTAACCTAT	60
GAAAGCACCC TCCAACAGGA TTTAAAAAAA ATCTTAGGGA TTGAAGAAGT CATAATGCTA	120
TCCACAAGCC CCATGGAATT ACGATTGGCC AATCAAAAGC TAGGCAATCG TTTCATTAAA	180
ACCTTACAAG CCATGAACGA ATTAGACATG GGTGCATTTT TTAACGCTTA CGCTCAAACA	240
ACCCAAAGAT CCCACCCATG CCAC	264

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 669 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370

GAAAAATCAA CGAGCAACTT GAAGAAGCCA AGCGTTTGGG GAAGCAAGTT GATATGCAAG	60
ATCGCCACTC ACAAAGCGAG ATCGATAGGC TTATGCGTGA AGCCAAAGAG CATGAAAGAG	120
AAGCTAAGAG GCGCTATGGT GAATATCTTA AGGATAAAAA TGATTGAAAT AAGCGAATGG	180
TTGCAAAAAC TAGACGATGC CTTAGATAAA GTTGTGCTA AAAAAGAGCC AGAGAGTTTT	240
CTCAAGCCGA TCATTTCACC AATAGAGGAC TACCAAAAGA GTGTCAGGCA AATTCAAGCG	300
CAATTACAG ACGCGCGGAA GTTCAATGAA GAGGGTGCTT ACCCTCAATT TTTAAGCTGT	360
GGTTTATTGC AAGTTAGGGG CAAAAATGGT GCTAACATGG AATTTTTATT GCCTAAAGTT	420
TATCCTTTCC CCCCTAAAAG CTGTATATA GAGCATGAAA AAGACGGGCA GTTTTTGAGA	480
GAAATGCTCA TCGCTTACT CTCCAGCGCG CCTTTAGTGC AATTGGAAGT GATCTTAATT	540
GATGCGTTGA GCTTGGGGGG CATTTTCAAT CTGGCCAGAA GGCTTTTAGA TAAAAACAAT	600
GACTTTATTT ACCAGCAAAG GATTTTGACC GAAAGCAAGG AAATAGAAGA AGCCCTAAAG	660
CATTTGCCA	669

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

966

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371

ACATGGGTGC	ATTTTTTAAC	GCTTACGCTC	AAACAACCCA	AAGATCCCAC	CCATGCCACT	60
AGCTATGGCG	TTTTTGGCGC	GAGTTTGAAT	ATGGAATTGA	AAAAGGCTTT	AAGGCATTAT	120
CTTTATGCGC	AAACTTCTAA	CATGGTGATC	AACTGCGTTA	AAAGCGTCCC	CTTATCCCAA	180
AACGACGGGC	AAAAAATCTT	ATTGAGCTTG	CAAAGCCCTT	TTAACCAGCT	CATAGAAAAA	240
ACCCTAGAAC	TAGACGAAAG	CCACTTGTGC	GCAGCAAGCG	TTCAAAACGA	CATTAAGGCG	300
ATGCAGCATG	AGAGTTTATA	CTCGCGCCTT	TATATGTCT			339

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372

CGAGCTTCAA	TGAAAAACTT	TTCCCCACTC	TATTGTCTTA	AAAAGCTCAA	AAAACGCCAT	60
TTAATCGCTC	TGAGTCTGCC	CTTGCTTTCT	TATGCGAATG	GCTTTAAAT	CCAAGAGCAA	120
AGCTTGAATG	GCACGGCTTT	AGGCTCGGCG	TATGTCGCTG	GGGCTAGGGG	TGCTGACGCT	180
TCTTTTACA	ACCCGGCTAA	CATGGGCTTT	ACTAACGATT	GGGGCGAAAA	CAGAAGCGAA	240
TTTGAAATGA	CCACCACCGT	GATCAATATC	CCGGCCCTTA	GCTTTAAAGT	CCCTACGACC	300
AATCAAGGCT	TATATTGCGT	AACAAGTTTA	GAAATTGATA	AAAGCCAACA	AAATATTTTA	360
GGCATCATCA	ACACTATAGG	GTTAGGCAAT	ATCCTTAAAG	CGCTTGCAAA	TACGGCCGCT	420
ACCAATGGCT	TATCACAAGG	TATCAATCGT	GTTCAAGGGG	TTATGAAC		468

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 651 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373

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GCGGATCGAG AGGATAAACT CTCTCACTCT ATAATCATGC GGTATTTTAT AAGCGCTTTT      60
TTATTATTTT TCATGACGCT TTTTTTTGTT TCTTGCTCTA AGCACCCCTT TTCTAAGCAA      120
ACCCCTAAGA CTAAGGAGCG GATCCGACAA GAAGAAGCCA ATAAAAAAG AGAAGAGACT      180
TTGAATGCCT TCGGCCAATT CAGACTCATT TACATTAACA CGCCGGTTT TCGCTTTTAT      240
GATTACGGCA CGATCAAAAC CGATAAAGAC CACAATACTG AAGTAACCC TTTATAAGCTC      300
AGCCAAAAG TGGGCGATAT TTACATGACT AAACGGAGCA TTTGTTTTAG CCAAAAATGT      360
TCGGCCAAAT GGATTGCTGC AAGGGATTTG TTTGGCAAGG TGAGCTATGG GGATTGTTT      420
GATGATATTG TTTAGGGGAG GGATATTTT AAAGGTTTAG GGAAACGCCA CCTAACCCCT      480
GAATATGTGA TCCAAAGGTT TCAAAAAGC GGGGAAATTA TCCTTTATGA AAGAAAAAAT      540
GGCCTGATTT CTTTCCAAA CTTGACTCAA AAAATTGCTA TTAGGATTGA ACCCTATGAG      600
CCTTCTTTGC AAGATTTAGA AGACAATGAA AACGCTGATA GCGAGCTTCA A              651

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(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374

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GAAATCGCTG AGATCGTGAG CCAATGGACG CACATCCCGT TCCAAAAAAT GTTCCAAAGC      60
GAAAAAATA GGGTTTTTAA CATTGAAAGC GAATTGCAAA AAAGGGTGGT GGGGCAAGAA      120
AAAGCGCTCA AAGCGATCGC TAAAGCGATT AAAAGGAATA AGGCTGGGCT TAGCGATAGC      180
AACAAGCCCA TAGGGAGTTT CCTCTTTTTA GGGCCAACAG GCGTGGGTAA AACCGAGAGC      240
GCTAAAGCTT TGGCGCAATT CTGTGTTGAT AGCGATAAAA ATCTTATACG AATTGACATG      300
AGCGAATACA TGGAAAAGCA CGTATCAGC CGTCTTATTG GGGCCGCTCC TGGGTATGTG      360
GGCTATGAAG AAGGCGGGCA AITGACCGAA GCGGTGCGCA GAAAACCTTA TAGCGTAGTG      420
TTATTAGATG AAGTGGAAGA AGCCCATCCG GATGTGTTTA ACTTCTTGTT ACAGGTTTTT      480
GATGAGGGGC ATTTAACC GA TAGTAAGGGC GTGAGGGTGG ATTTCAAAAA CACGATTTTG      540
ATTTTAACCA GCAATGTGGC TAGCGGCGCG CTTTTAGAAG AGGATTTGAG TGAAGCCGAT      600
AAACAAAAAG CGATCAAAGA GAGCCTGAGA CAATTCTTCA AGCCGGAATT TTAAACCGC      660
TTAGATGAAA TCATCTCCTT TAACGCCCTA GATAGTCATG CTATCATC              708

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(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

968

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...777
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375

GTGAGGTTTT	GTTATTCTAA	AAAATATAAA	AAAACGATTA	TTTTAAAAAA	GGATTGGATG	60
ATGTTTGATA	ACACGCTTAT	CAATTTATTT	GAGACAGCGC	CTCTTTTAAC	TTCGCTTTTA	120
GCTGGGATTT	TAACTTTTTT	AAGCCCTTGC	GTGTTGCCCT	TGATCCCGGC	GTATATGTCT	180
TATATTTTCG	AAATTTCTTT	AGAGGATATT	AAAGATGGTA	AGGCTAAAAG	GGTTTCGGTT	240
TTTTTAAAAA	CCTTGATGTT	TGTGGTGGGG	TTTTCGCTCG	TGTTTTTGGG	CGTGGGCATG	300
TCTATGGCCA	AGCTTATCCA	TAGCTTTTCG	TTTTCTGGGG	TGAATTATAT	CGCTGGGGGG	360
ATTGTGATCC	TTTTTGTTTT	GCATTTTTTA	GGCGTGTTC	GTTTTGCGCT	TTGTATATAA	420
ACCCAAAGCG	CTGGTTTAGC	GAGCAAATCT	AACAGCATGC	AGCGCTTTTA	CCCCTTTCTT	480
TTGGGCATGA	TTTTCGCTTT	GGTTGGACG	CCATGCATCG	GGCCGATATT	CACTTCTATA	540
GTGATCATGA	GTGCGAGTAA	GGACGCTTAT	GGCTTAATGC	TTATGGTGGT	GTTTGTAAATG	600
GGCTTGGCGA	TCCCTTTTGT	ATGGGTGGCT	TTAATGCTAG	AAAGAGCGCT	TTTGTTTTTA	660
AAATCCTTAA	GAAAATACAA	CCGCGCGATT	GAAATTGTTT	CAGGTTGGT	GCTTATTTTA	720
ATGGGAATAT	TGATCATGAC	AAATCTTTTA	GAAAGCCTAA	CTAATTTTTT	ACAAAAT	777

(2) INFORMATION FOR SEQ ID NO:1376:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...594
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376

ATAGGAGGTG	CGCATGCGTT	TTTATATTAT	CTTACATTTT	TGTTTATTGT	GGGTTTTGGC	60
GTGTTTGTIT	ATAGTATTGA	TCCGCAAGCT	TACGCTTTCA	ATTTAGGGAG	CTATAGCTTT	120
AACCTCCCCA	TTGCCGTATG	GCTTATGGGC	GTTTTGGGCA	TGTTGCTTTT	TTTTTCATGG	180
GTTTTTTTAT	TCAAGCACAA	TCTCAGCCAT	AAAATCCGCT	TATACCATGA	AAAAAAGGAT	240
TTTGACAAAT	TGCTCAAACA	AATCCTATCC	CAAGACACCC	AAAAGACTTT	TTTAAAAACA	300
AAATTTAAAA	GCGATCTCGC	TAAAAACCTC	TCTCAAATCT	TAGCCCGCTA	TGATTTAAAA	360
GCTGATTTAA	ACACGCCAAA	TAGCGGGTGC	GAAAAAGTGG	ATAACCTTTT	TAAACATTAC	420
CACATATATG	AAAATAACAC	CCTTGAGCCT	AAAGATCACG	CTAAACATTC	CCTAGCTTAT	480
GAGCATGCTT	ATTTTTCTAA	ACGCTTGAAG	GCTTTCATTC	ATAACGATTT	GAAAAACGCC	540

SUBSTITUTE SHEET (RULE 26)

969

TTTGAAGTTT TAACAAACGC GCAAATCCCT TTGGAATTAC GCCGCTACGC CTTA

594

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377

CAAGATAAGG	GGTTATTATT	GAGTGTAGCA	CTACCTAACT	CAAACAACGC	CTCTCAAAAC	60
AACATTTTAA	GCCTTTCTGT	CCITCACAAC	CAGATTAAAA	TGTCTTATGG	TAATAAAGTG	120
ATGGACTTTA	CCCCTCCCAC	CTTACAGGAT	TACATTGTGG	GCATTCAAGG	ACAAAGCGCA	180
CTCAATCAAA	TTGAAGCTGT	TGGGGGGAAT	AACGCTATCA	AGTGGCTTTC	AACATTGATG	240
ATGGAGACTA	AAGAAAACCC	GCTTTTTGCG	CCGATTATT	TAGAAAACCA	CTCTTTAAAT	300
GAAATCTTAG	GCCTAACAAA	AGATCTTCAA	AACACCGCAA	GCTTGATTTC	TAACCCCTAAT	360
TTTAGAAATA	ACGCTACCAG	CCTTTTAGAA	ATGGCGAGTT	ACACCCAACA	AACCAGCCGT	420
TTGACAAAAC	TCTCTGATT	TAGGGCTAGA	GAGGGAGAGT	CCAATTTTTC	AGAGCGCTTG	480
TTAGAGCTTA	AAAACAAGCG	TTTTAGCGAT	CCTAACCCCTA	GTGAGGTTTT	TGTCAAATAC	540
TCTCAACTCA	GCAAACACCC	CAATAACCTT	TGGAFTCAAG	GGGTGGGAGG	AGCGAGCTTT	600
ATTTCTGGGG	GCAATGGCAC	GCTTTATGGC	TTGAATGTGG	GCTATGACCG	ATTGGTTAAA	660
AGCGTGATCC	TTGGGGGTTA	TGTGGCTTAT	GGCTATAGCG	GTTTTAACGG	GAACATCATG	720
CATTCTTTGG	CTAATAATGT	GGATGTGGGG	ATGTATGCGA	GGGCTTTTTT	GAAAAGAAAC	780
GAATTCACCT	TGAGCGCGAA	TGAAACTTAT	GGAGGCAATG	CGAGTCATAT	CAATTCTTCT	840
AATTCCTTGC	TCTCTGTGTT	GAACCAACGC	TACAACCTACA	ACACCTGGAC	AACGAGCGTG	900
AATGGGAATT	ACGGCTATGA	TTTCATGTTT	AAACAAAAAA	GCGTGGTGCT	AAAACCTCAA	960
GTGGGCTTGA	GCTATCATTT	CATAGGCTTG	AGCGGGATGA	AAGGTAAAAT	GCAAAATCCA	1020
GCTTACCAAC	AATTCGTGAT	GCATTCAAAC	CCTTCTAACG	AATCGGTTTT	AACGCTCAAC	1080
ATGGGGTTAG	AGAGCCGTAA	ATATTTTGGT	AAAAATTTCCT	ATTATTTTGT	AACGGCGAGG	1140
TTGGGTAGGG	ATCTTTTGAT	CAAAGCTAAA	GGCGACAATG	TGGTGCGTTT	TGTGGGTGAA	1200
AACACTTTAT	TGTACCGCAA	GGGGGAAATT	TTTAACACTT	TTGCCAGCGT	GATCACAGGA	1260
GGCGAAATGC	ATTTGTGGCG	TTTGATGTAT	GTGAATGCGG	GGGTGGGGCT	TAAAATGGGC	1320
TTGCAATACC	AAGATCTTAA	TATCACTGGG	AATGTGGGCA	TGCGAGTGGC	GTTT	1374

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

970

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378

ACGATACTAT	CCCCAGGGGC	TAAAGCTAT	AAGTATTGGG	AAGGCATGGG	CATGTCTCAT	60
ATTATTAAGA	GCATTGAAGC	TTTAGATGAC	TATACCATT	GATTCACGCT	TAATGGGCCA	120
GAAGCCCCGT	TTTATGCGAA	TTTGGGCATG	GACTTTTAA	GCATTTTGAG	TAAGGATTAC	180
GCTGATTACT	TGGCTCAAAA	TAATAAAAA	GACGAGTTGG	CTAAAAAACC	TGTTGGGACA	240
GGGCCTTTCA	AATTCTTTTT	GTGGAATAAA	GATGAGAAAA	TCATTCTGGT	TAAAAACCAG	300
GATTATTGGG	GCCTTAAAGC	GTATTGGAT	AAGGTGGTGG	TGCGCACCAT	TCATAATTTT	360
TCCACTCGCG	CCTTAGCGTT	AAGAACCGGT	GAAATCATGC	TCATGACCGG	GCATAATCTC	420
AATGAAGTGG	AGCAATTAGA	AAAACCTCAT	AATATCGTGG	TGGATAGAAG	CCCTGGGTTG	480
ATCGCCAACT	GGCTTTTCATT	GAACACGCAA	AAAAAGTATT	TTAATAACCC	TTTGGTGCCT	540
TTGGCTATCA	ATCATGCCAT	CAATGTTGAT	GATTACATCA	AGGTGATTTA	TGAAGGTTTT	600
GCTCAAAAAA	TGGTCAATCC	CTTCCCGCCC	ACCATATGGG	GTTATAACTA	TAATATCAAA	660
CCCTACGAAT	ACGATTGTAA	AAAGGCTAAG	GAGTTGTGTA	AACAAGCGGG	CTATCCTAAC	720
GGCTTTAAAA	CCAATATTG	TACATCTTTA	CTC			753

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2637 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379

ATTTCATATTA	AACGAATTTT	TTTACTTAAA	AACACCCCAT	TTAACCCGCC	ATTATTCCTC	60
CACATTGCCC	CACTCAAACC	ATTTCATGATT	ATTATTAAC	TGTTTGGAA	TACTTTTAGC	120
TTGTTTGTTA	AAAAAACCAA	TAAGGATTG	ATCATGCGCG	TTACCTTTGG	CTCCAAATAC	180
AACCAATGA	ATCACTACCA	AAACGCTTTA	CAAAATAAAA	TCAACGACGC	TAACACGCAG	240
ATCGCTTCAG	GGCTAAAAAT	CCGTTATGGT	TATCAAAACA	GCGACATTAA	CAACCAGAAT	300
TTAAATTC	AATACGAAGA	AAACACCTTA	GATCAAGGCA	TTGATGTGGC	TCAAAACGCT	360
TACACTTCAA	CGCTCAATAC	CGACAAAGCC	TTGCAAGAAT	TTTCTAAAAC	GATGGAGGCG	420
TTTAAACCA	AACTCATCCA	ATCCGCTAAC	GATGTGCATT	CAGAGACTTC	TCGCGCCGCT	480
ATCGCTAACG	ATTTAGAACG	CTTAAAAGAG	CATATGATAA	ATGTCGCTAA	TACCTCCATA	540
GGGGGGGAAT	TTTTATTGG	AGGCAGTAAG	GTGGATAGAC	CCCCATTGA	TAGTAATGGG	600
AAATACCATG	GCAATGGCGA	AGATTTAAAC	GCGCTTATTA	GCTCTGATAA	CCTTGTGCCT	660
TATAATATCA	GCGGGCAAGA	TTTGTTTT	GGCACCATA	AAGACAAACA	CAAACTCATT	720
ACCACCAACA	TTAAATTACT	CAATCAAAC	AAGCTCCACC	CTGATGTGAT	GGACGCTTTA	780
GAGCATTCTT	CATTGCCTGA	AGAAGTTTC	ATTAAACCA	GCGATACCTT	GCGAGAACTC	840
ATCGGCGATA	ACGATAAAAA	CCCCACCAAT	GACCCTAAG	AGTTTTTTTA	TTTGCAAGGC	900
ATTAGGCCTG	ATGGCTCTAG	TTTTAAAGAA	AAATTCGCGT	TGGATAAAGC	CTATCAAAAC	960
CAAGAAAGCG	CGACTAAAGT	GAGCGATTTG	TTGGATAAAA	TCGGGCATGC	TTACGGGAAC	1020
ACTTCGCAAA	ATAAAGTCGT	GGATGTGAGT	TTGAACAATT	GGGGGCAAA	TGAGATTAA	1080

SUBSTITUTE SHEET (RULE 26)

971

AACCTAACCC	CCGGCAGTGA	AAATTTGGAT	TTTCATTTGA	TTTCTAGCGA	TGGGGATTTT	1140
GACGATTTAG	ACGCCCTGCG	TTTCGAGCGGT	AAAAGGGTTA	CTGAATATGT	CAAAAGCGCG	1200
TTTGTAACGG	ATAGGAGTTT	GAGCCAAGTT	AAAGCGGTGC	CTAACATGTA	TAACCCATAA	1260
GTGCTTGAAA	TCCCTAGCGT	GTTTGTGACT	AAAGACAATG	TTTTAGCTAA	CAAAAACACC	1320
AAGTTGAGCG	AGATTTTTGG	CGATAAGGTG	GAAACTTTAA	AAATCAACGC	CAGCCGTTTG	1380
GGCGATGAAA	GCGCTATTAA	AATCCCAAAC	CTCCCTATTA	ATTGAGATAT	TCCCATTCCT	1440
TTAGATGTGA	AAAACCTAC	GATTAAAGAT	TTGAAAGACG	CGATTAAAGA	ACGCTTCAAT	1500
AATGAAGTGG	ATGTGGAAAT	TGAAACGAAC	GGGCGTTTGA	GGATCATTGA	CAATTCTTCT	1560
AAAGAATCGC	CTATTTCCTT	TGCCTTAAGC	ACCCTGGATC	AAAAAGGGCT	AGAAGTGGCC	1620
GGTATCCCCA	CTAATAACGC	GAGCGAATAC	CAAAAAACCT	ATTTCAATAA	AGAAGGGGCC	1680
AAATTAGAAA	GCAATGTTGC	CCAAACCGCT	CAAAATGATG	CGGCTAATGG	CTCTACTAAA	1740
CTGAGTGAAG	TCTCTAAGGG	GAGTTTGGAA	AATAGCGTTT	TTAACATGAA	ATTAAACGAT	1800
GTGAATGGTT	CGTTTTTAGA	AGCGCAAATA	AACCTGGATA	ATAATGGGGC	TTTTTTGAGT	1860
TTGCCTAATG	GCGTTAAAT	CCCGCTTTAT	GACCCACAA	CCGCTGATAT	TCAAGCGTCT	1920
AAACCCAATG	AAGTCACTTA	CAGGCAGCTC	ATGGATGCGA	TGAGTATCGC	GCTCAATTAC	1980
AGCAACACTG	ATCCTGCAAT	CTACCAACAA	ATCAGCGATA	ACCCTACTTC	AAAAGAAAGC	2040
AAGGAGCGAT	TCATTGAATT	GTTAAACAA	GCTAAAGACA	ACCTTTCTAT	TAATTTGAAT	2100
GAAGAGGGTA	AAGTCATTAT	CCAAGACAAC	ATGCATTCAA	ACACCAAAAT	GCAGTTCATG	2160
CTTTTTGATA	AAGACGCGAA	TGATTTTTCT	CAAAACGCCT	TACACAGCGA	CAAACCAAGC	2220
CTTAAATTAA	ACGCTAATAA	CGCCCTAATT	ATTGACAAGC	CAAGCGTGAA	TTTTTTTGAT	2280
CAATTAGAAA	ATATTATCAC	TTCTGTAAGA	AAAGGGATTT	ATCGCCCAGA	CGCTTTAGGG	2340
GATACCTTAT	CTAGCGACAT	GCGTAATTTA	GGCATTCAAA	ACGGCATCAC	CCTTATAGAT	2400
CACCTGAGCG	ATCACATAGA	AAAAATGATC	GCTAAAAACG	GCGCTCATGG	TAAGGCATTT	2460
GAAAACATCA	TCAGGCGTAA	TGAAGTTTTA	AAAACACAAG	TTCAAAGCAT	TCGTGGGGAA	2520
ACGACCGGCA	CGGATATGGC	AGAACTTAT	AACAAGTTT	CCAATCTCAC	TAACACTAT	2580
AACGCCGTTT	TGGCTTCCAC	GAACAAAATC	AATAATCTGT	CTTTAACGAA	GTATTTA	2637

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380

AGGATTGATC	AAATTAAAT	TATGAAATG	GTGAGTCTTA	TTGTAGCGTT	AGTTTTTTGT	60
TGTTTTTTAG	GGGCTGTAGA	GTTGCTGGA	GTTTATCAAA	CTCAAGAATT	TTTATACATG	120
AAAAGCTCTT	TTGTGGAGTT	TTTTGAGCAT	AACGGGAAGT	TCTATGCCTA	TGGTATTTCT	180
GATGTGGATG	GCTCTAAAGC	CAAAAAGAC	AAACTCAATC	CTAACCCAAA	GCTAAGGAAT	240
CGCAGCGATA	AAGGCGTGGT	GTTTTTAAGC	GATTTGATTA	AGGTTGGGGA	ACAATCTTAT	300
AAAGGCGGTA	AGGCGTATAA	TTTTTATGAC	GGCAAGACCT	ACCATGTGAG	AGTCACTCAA	360
AATTCAAACG	GGGATTTGGA	ATTCACTTCA	AGCTATGACA	AATGGGGGTA	TGTGGGCAAT	420
ACCTTCACTT	TGAAACGCGT	GAGGGGTGCC	GAAATCAGTA	TTTTAAAGCT	CAAGCGTTTT	480
AATCTCATGC	GCTCTTTTTA	CAGGCAGACC	CACCTTTTTT	CTATTGGTAA	GGCCTACGCG	540
ACA						543

(2) INFORMATION FOR SEQ ID NO:1381:

SUBSTITUTE SHEET (RULE 26)

972

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381

AAGGATTTAA	GCAAGATGTT	TGTGGTTTTT	ATAGAAGGTT	TGGTTTTAGC	GATTTCTTTG	60
TGCCGCGCGG	TGGGGCGCGA	ATCCTTGTTT	ATTGTGGAAA	GGGGGATGGC	TAGGAATTAT	120
GTGTTTTTGA	TTTGGCCTTT	GTGTTTTATG	TGCGATATTG	TCTTAATGAG	CATGGGCGTG	180
TTTGGCGTGG	GGGCTTATTT	CGCTAAAAAC	CTTTATTTGA	GCTTGTTTTT	GAATTTATTT	240
GGGGCAGTTT	TTACCGGATT	TTACGCTTTT	TTGGCTTTAA	AAACCCTTTT	TCAAACCTTT	300
AAAAAAAAGC	AAGTCCAAAC	CCCTAAAAAA	TTATCCTTAA	AAAAGACCTT	ATTATTCAC	360
TTAGGCGTTA	CCTTACTCAA	TCCTCAAGTG	TATTTGGAAA	TGGTGTTTTT	AATTGGCGCG	420
AGCGCTATGT	CTTTTAACCT	AGTGCAAAAA	TTCGTCTTTC	TAGCTGGCAC	TTTATCGGCT	480
GCCTTTTCTT	GGCTTTTATT	GTTATGCACC	ATGTCCTTAC	GCTATGGCTC	TAAACTTTTG	540
AACAACCAAA	AAATCTTTAT	GGGCGTGAAT	CTCTTTGTAA	CCGCTATCAT	GGAACGCTC	600
AGCGTTACTT	TATTCAGGGA	TTTTTTAGCG	TTATTGAGCA	AAACC		645

(2) INFORMATION FOR SEQ ID NO:1382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382

ATGGATATTT	TAAAAGCAGA	GCATTTAAAC	AAACAGATTA	AAAAAACCAA	AATCGTTTCA	60
GATGTTTCTT	TAGAAGTGAA	AAGCGGCGAA	GTGGTGGGGC	TTTTAGGGCC	TAATGGGGCG	120
GGTAAAACCA	CCACCTTTTA	CATGATATGC	GGGCTTTTAG	AGCCTAGTGG	GGGGAGCGTT	180
TATTTAAACG	ATGTGGATTT	AGCTAAATAC	CCCTTACACA	AGCGTTCTAA	CTTGGGCATA	240
GGCTACTTGC	CCCAAGAATC	CAGTATTTTT	AAAGAATTGA	GCGTGAAGA	GAATTTGGCC	300
CTAGCAGGGG	AGAGCACTTT	TAAAACTCT	AAAGAGAGCG	AAGAAAAAAT	GGAAAGCTTG	360
CTTGATGCTT	TTAATATCCA	AGCCATAAGA	GAGCGCAAGG	GCATGAGCTT	GAGTGGGGGA	420
GAAAGAAGGC	GCGTAGAAAT	CGCTAGGGCT	TTAATGAAAA	ACCCTAAATT	CGTGCTGTTA	480

SUBSTITUTE SHEET (RULE 26)

973

GATGAGCCTT	TTGCGGGCGT	GGATCCGATT	GCGGTGATTG	ACATTCAAAG	AATCATTGAA	540
AGCTTGATTG	GATTAAACAT	TGGCGTGTG	ATTACTGATC	ACAATGTGCG	AGAGACCTTG	600
AGCGTGTGCC	ATAGGGCGTA	TGTGATCAAA	AGCGGCACGC	TTTTAGCGAG	CGGGAACGCT	660
AATGAAATTT	ATGAAAACGC	TTTGGTGCCT	AAGTATTATT	TAGGGGAAAA	TTTTAAGGTA	720

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383

AACACTGGTT	TGTGGCACTC	TTGGGGTTTG	GCTCCAGCGC	TTTTGGAAC	GCAACTGCC	60
AAACATGCTC	ACCAATTTT	TCAAATCTTC	TTTTCCTT	AAAAGCCCTT	CAAACAAATG	120
ATCGTTATTG	TGGAGTTGCT	TGTCAATTTT	ATCTTTAATC	TCTTTCACGC	CATACATGTT	180
GGGGTTAAAA	TGATAGATAA	TATCAAATC	CCACTTAGAC	GCATAAAAT	GCGCGCTCTC	240

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384

ATTGATCTAG	GCGTGATAGA	GACCATCCCC	AAACACTCTA	AGATTGTTTT	ACCCGGGGAG	60
GCGTTTGATA	GTTTAAAAGA	GGCGTTTGAT	AAAATTGACC	CCTATACTTT	CTTTTTTCCA	120
AAATTTGAAG	CCACTAGCAC	TTCTATTTC	GATACTAACA	CGCAGAGGGT	GTTTGAAACG	180
CTCAATAACA	TTAAACAAA	TCTTATAATG	AAATATAGTA	ATGAAATCC	AAACAATTTT	240
AACACTTGTC	CTTACAATAA	TAATGGTAAT	ACAAAAAATG	ATTGTTGGCA	AAATTCACC	300
CCACAAACCG	CAGAAGAATT	CACCAATTTA	ATGTTGAACA	TGATCGCTGT	TTTAGACTCC	360
CAATCTTGGG	GCGATGCGAT	CTTAAACGCT	CCTTTTGAAT	TCACTAACAG	CTCAACAGAT	420

SUBSTITUTE SHEET (RULE 26)

974

TGCGATAGCG	ATCCTTCAAA	ATGCCGTAAAT	CCCGGAGTAA	ATGGGCGTGT	TGATACTAAA	480
GTCGATCAAC	AATATATACT	CAACAAACAA	GGTATTATTA	ATAATTTTAT	AAAAAAAATA	540
GAAATTGATG	CGGTTGTTTT	AAAAAATTCA	GGGGTTGTAG	GGTTAGCCAA	TGGATATGGC	600
AATGATGGTG	AATATGGCAC	ATTAGGGGTA	GAAGCCTATG	CTTTAGATCC	TAAAAAACTC	660
TTTGCGCAACG	ACCTTAAGAC	TATCAATTTA	GAAGATTTAA	GAACCATCTT	GCATGAATTC	720
AGCCACACTA	AAGGCTATGG	GCATAACGGG	AATATGACCT	ATCAAAGAGT	GCCGGTAACG	780
AAAGATGGTC	AAGTGGAAAA	GGATAGTAAT	GGCAAGCCAA	AAGATTCTGA	TGGCCTTCCC	840
TATAATGTGT	GTTTCGCTTA	TGGGGGATTC	AATCAGCCCC	CTTTCCTTAG	CAACTACCCT	900
AATTCCATCT	ATCACAATTG	TGCGGATGTC	CCGGCTGGCT	TTTTAGGGGT	AACAGCAGCG	960
GTTTGGCAGC	AGCTCATCAA	TCAAAACGCC	TTGCCGATCA	ACTACGCTAA	CTTGGGGAGT	1020
CAAAACAACT	ACAACCTAAA	CGCTAGTTTA	AACACGCAAG	ATTTAGCCAA	TTCCATGCTC	1080
AGCACCATCC	AAAAAACCTT	TGTAACCTCT	AGCGTTACCA	ACCACCATTT	TTCAAACGCA	1140
TCGCAAAGTT	TTAGAAGCCC	TATTTTAGGG	GTTAACGCTA	AAATAGGCTA	TCAAAACCTAC	1200
TTTAATGATT	TCATAGGGTT	GGCTTATTAT	GGCATCATCA	AATACAATTA	CGCTAAAGCT	1260
GTTAATCAAA	AAGTCCAGCA	ATTGAGCTAT	GGTGGGGGGA	TAGATTGTGT	ATTGGATTTC	1320
ATCACCACCT	ACTCCAATAA	AAATAGCCCT	ACAGGCATTC	AAACCAAAG	GAATTTTTCT	1380
TCATCTTTTG	GTATCTTTGG	GGGGTTAAGG	GGCTTGATA	ACAGCTATTA	TGTGTTGAAC	1440
AAAGTCAAAG	GAAGCGGCAA	TTTAGATGTG	GCTACCGGGT	TGAACCTACC	CTATAAGCAT	1500
TCTAAATATT	CTGTAGGGAT	TAGCATCCCT	TTAATCCAAA	GAAAAGCTAG	CGTCGTTTCT	1560
AGCGGTGGCG	ATTATACGAA	CTCTTTTGTT	TTCAATGAAG	GGGCTAGCCA	CTTTAAGGTG	1620
TTTTTCAATT	ACGGGTGGGT	GTTT				1644

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385

GATCATAGCT	TTAATATTCA	AAATAGTATA	AAAAGGAAAG	TCATGTATGC	GGCTCATCCT	60
ATTAAACCCA	TAAAAGCCCC	TAAACTCAAA	TCTCAATTTT	TAAGGCGTGT	GTTTGTGGGC	120
GCGTCCATTA	GGCGCTGGAA	TGACCAAGCA	TGCCCTTTGG	AATTTGTGGA	ATTAGACAAG	180
CAAGCCCATA	AAGCGATGAT	TGCGTATCTG	CTCGCTAAAG	ATTTAAAAGA	TAGGGGTAAA	240
GATTTAGATT	TAGATCTTTT	AATCAATAT	TTTGTCTTTG	AGTTTTTGGA	GCGCTTGGTT	300
TTAACCGATA	TTAAACCCCC	TATTTTTTAC	GCCCTCCAAC	AAACGCATAG	TAAAGAGTTA	360
GCTTCCTATG	TTGCGCAAAG	TTTGCAAGAT	GAAATCAGTG	CGTATTTTTC	TTTAGAGGAA	420
CTCAAAGAGT	ATTTAAGCCA	CAGGCCTCAA	ATTTTAGAAA	CTCAAATTTT	AGAGAGCGCG	480
CATTTTATAG	CGTCTAAGTG	GGAGTTTGAT	ATTATCTATC	ATTTTAACCC	CAACATGTAT	540
GGCGTGAAAG	AGATTAAAGA	TAAATTTGAC	AAGCAACTCC	ACAATAACGA	TCATTTGTTT	600
GAAGGGCTTT	TTGGGGAAAA	AGAAGATTTG	AAAAAATTGG	TGAGCATGTT	TGGGCAGTTG	660
CGTTTCCAAA	AGCGCTGGAG	CCAAACCCCA	AGAGTGCCAC	AAACCATGTT	TCTAGGGCAT	720
ACTTTATGCG	TGCGGATTAT	GGGGTATTTA	TTGAGTTTTC	ACTTGAAAGC	TTGTAAAGC	780
ATGCGGATCA	ATCATTTTTT	GGGCGGGCTT	TTCCATGATT	TACCCGAAAT	TTTAACCCGA	840
GACATTATCA	GCCTCATCAA	ACAAAGCGTT	GCAGGGCTTG	ATCATTGCAT	TAAAGAGATT	900
GAAAAAAGG	AAATGCAAAA	CAAAGTCTAT	TCCTTTGTGT	CTTTGGGCGT	TCAAGAAGAT	960
TTGAAATATT	TCACCGAAAA	CGAGTTTAAA	AACCGCTACA	AAGACAAGTC	TCATCAAATC	1020
GTTTTCACTA	AAGACGCTGA	AGAATTATTC	ACGCTTTATA	ATAGCGATGA	ATATCTTGGG	1080
GTTTTCGGGG	AGCTTTTGAA	GGTGTGCGAT	CATTTGAGCG	CGTTTTTAGA	AGCCCAAATC	1140

SUBSTITUTE SHEET (RULE 26)

TCTCTTTCTC ATGGCATTTC TAGCTACGAT TTAATCCAAG GAGCTAAAAA CCTTTTAGAA 1200
 TTGCGATCCC AAACGGAAGT GCTTGATTTC GATTAGGGA AATTGTTTAG AGATTTTAAG 1260

(2) INFORMATION FOR SEQ ID NO:1386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386

AATATTACAA	TCAAGGATAG	AACGATGAAA	ACAAATGGTC	ATTTTAAGGA	TTTTCATGG	60
AAAAAATGCT	TTTTAGGCGC	GAGCGTGGTG	GCTTTATTAG	TGGGGTGTAG	CCCGCATATT	120
ATTGAAACCA	ATGAAGTTGC	TTTGAAATTG	AATTACCATC	CAGCTAGCGA	GAAAGTTCAA	180
GCGTTAGATG	AAAAGATTTC	ACTTTTAAGG	CCAGCTTTCC	AATACAGCGA	TAATATTGCT	240
AAAGAGTATG	AAAACAAATT	CAAGAATCAA	ACCACGCTTA	AAGTTGAAGA	GATCTTGCAA	300
AATCAGGGCT	ATAAGGTTAT	TAATGTGGAT	AGCAGCGATA	AAGACGATTT	TTCTTTTGCG	360
CAAAAAAAG	AAGGGTATTT	GGCTGTCGCT	ATGAATGGCG	AAATTGTTTT	ACGCCCCGAT	420
CCTAAAAGGA	CCATACAGAA	AAAATCAGAA	CCCGGGTTAT	TATTCTCCAC	TGGTTTGGAT	480
AAAATGGAAA	GGGTTTTAAT	CCCGGCTGGG	TTTGTCAGG	TTACCATACT	AAAGCCTATG	540
AGTGGGGAAT	CTTTGGATTG	TTTTACGATG	GATTTGAGCG	AGTTGGACAT	CCAAGAAAAA	600
TTCTTAAAAA	CCACCCATTC	AAGCCATAGC	GGAGGGTTAG	TTAGCACTAT	GGTTAAGGGG	660
ACGGATAATT	CTAATGACGC	AATTAAGAGC	GCTTTGAATA	AGATTTTTCG	AAGTATCATG	720
CAAGAAATGG	ATAAGAAACT	CACTCAAAGG	AATTTAGAAT	CTTATCAAAA	AGACGCCAAG	780
GAATTAAAAA	ACAAGAGAAA	CCGA				804

(2) INFORMATION FOR SEQ ID NO:1387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387

SUBSTITUTE SHEET (RULE 26)

976

TCAAATTTTA	AAAAAGGATT	TTTTATGTTT	AAAAGCAGAT	TAAATTCATG	GATTTTATTA	60
GGGATTTTAG	GGGTTTTAGT	GGTGGTTT	TGGGATGTCA	TAAAATACAA	AATAGAAGAT	120
TTGCAACATG	ATCATTATCT	ATCACAAAGT	AAAGAAAGGG	AAGAATATTA	TAAAAACCAC	180
ATAGAAGAAG	CTTTGAAAAA	GGATAGCGAA	TGCTTTGAAA	AAGGAGGCGA	TAAAGTGGAT	240
TGCTCGGCTG	CTATGAGAAT	AGCTGCTGGT	GAAAGAAATA	GAAGAATGTT	AGAGATTAAA	300

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388

AAATTATTTT	TAGTTATAAT	TTTTCAAAAA	ACCTTAAGAG	AAATCATGCA	AGATTTACAA	60
CATTTCAAAA	ATGATATTAC	GCTCATTCTA	TCTAAAGACA	GATTAGATAC	TTATGACAGC	120
CTAGAGCAAT	ACAAAGAAAA	TTTAAACTC	ATTGCTTTCA	TCACGCCTAA	AATTTCTAAC	180
TTAGAAATTT	ATTTACGCAA	CGCTTTAGAC	TATTGCCTGA	CTCAAATGAA	AGGGAGTGAA	240
TGGGTGTTTA	ACGAAAGCGT	TTTAACCCCT	TTAATCAAAG	AATTAAAAGA	AAAGAAAAAA	300
GAAATCACGC	ATTCCTTAAT	CTTATCTAAA	ATGCTTTTAG	GGGCAGTGAT	CAGGCTTATT	360
TTTTGTATA	AGTTAGAGGG	GGTAATATTA	GATTTAAAGC	GCATCAATTT	CAAATCCTAT	420
TACCCCAATA	ATAAAATGCG	ATTATTATC	AACAATAAGA	AAAATCCATT	ATCTAGTGCT	480
TCAAAGGTTT	ATATTGCTTT	AAACTTGCTA	TGGACAATTA	GAAATCGTGC	GTATCATTGG	540
GAAAATTTAC	TCAAAATCCA	ACCGAACAAAG	CGCCCCACGCA	TTACGACTTA	TTTCATTGGG	600
TTAAAGACA	ATGATAGGGC	AAGAATTCCT	ATGAATATCA	GTGTAGAACC	AAGTAAATC	660
GTCTTGTTTT	TAGATGATTT	AATTAAAAGC	ATCGGAAATA	AAGACTTGGA	AGATTTAAGT	720
AGTTTG						726

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389

GGCATGAAAG	CGTTGAAGAC	TTTTTTAAAA	AAATCCCTTA	TTCTGTTACT	AGCAATTGCC	60
TTAAACCACT	TAAACGCTGT	GGCTATGATT	GTGGATAATC	CTACGCAGAA	CGCTTGGAAT	120
GGTGCTAAAA	GAGCATGGGA	TGAAAGCAAG	TGGGCTAAAC	ATTTAGCCAC	TATTACTGAA	180
AGGATCAAGC	TCGCTCAAGA	CACATTAGAT	AGGGCTAATC	AGACGCTTAA	TTCCATCAAC	240
AAAGTGAATG	ATGTTTTTGA	CAAAACCAAT	CAATTTCTAA	CAGGCAGTAT	TTTAAGCATC	300
CCCAATCCCA	TGCAGTATGT	AGAAAAATC	CAAAGTTTTG	CCAAGCAAGT	TCAAGCCAAT	360
ACTGAAAGGA	TCAAAGAAAA	TGCACAAAAC	TATGATATAC	GCAATCAAAT	TGCAGCCAAA	420
CGCATCTCTG	AAAAATGCCC	TGAATCAAT	TGGGATGTCA	GTCAAGACGC	GAGCCCTACA	480
GAGAAAAACT	TACACCAATT	TTTCACGAGC	AAGGGGAAAAG	AAAGCGCTAA	CACAAAGGCT	540
CTAAAGGATT	TTGCTAACGC	CATAGGTAAC	ACTCAAATCA	GCACGGCGAA	CGATTTAGGA	600
GCTGGACTTA	GAGGCAGAGC	CTTATTAGAA	TACATTGCA	TTCAAAAAGG	CAATTTAGAA	660
GCGGCTAAAA	AAATCCAATT	ATTAGACAGC	CAAATGACTT	TAGCTCTACT	CAATAACGAC	720
TATACGGCTT	ATGAAAAACT	TAGAGCTGAA	AAAGAAGAAT	TAAAAAGACA	AATCGCTTCA	780
AATGTGTATG	CGAAAGTCAA	ACAGCTTGTT	GTAGCTTCCC	AAGATAGAGC	GTTTAGTCAA	840
ATGGATAATG	AGTTGGGCGT	TAAACTTTTT	GGGTTCAACG	ATGAGAATGT	TAAAAAAGGT	900
TATTGCAAGA	AAGAAAACAG	AAATGGCAAA	AGCGAGTGCA	TCCCTAACAT	GCTCAATGTT	960
AATCGCTTAA	AAGCGCAATT	TGATGAGCTT	AATTTAGATT	ATAGTAGGGA	TATTGCTGGT	1020
AAAAAAGGTG	AAGCAGCCGC	TAAAGTGTTT	AATGACTACA	AACACCGATT	CCAACAATTA	1080
AGCGTAGAAA	CTGCTTTAGA	AATCGCTCAA	AATTTAAGTT	TTATGAATAA	GACGCTAGGT	1140
TTAATGGTGC	AAATGCAAAG	CTATGCATTC	AAGCAACAAA	TGGGCTATTT	TGAAGATATT	1200
ATTCCTGCTG	ACGCCCTAAA	AGATGACAAA	GAGCATCAAG	AAAATCTTGA	ACAAAAACAA	1260
CAAGAAATAG	AGAAAAGTCTA	TAGGGCTAAA	TTAGACGCTT	ATGGTTTCCC	TAATGGTAGT	1320
GTAGGAAAGG	CAAGTGGCGT	GAATTCAAAT	AGTAATAATG	AAGCCCCAAG	CTCTGATAAT	1380
ATCCAGTCGT	TTAATCCGTA	T				1401

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390

AGATTAAATA	ACATGGCCGC	TCCACTACTT	GCTCTGCCCT	TTCTTTCTAA	CCCTTTAGTG	60
CTTGGTGCTT	TAGCTGTCAT	AGGAGTGGGT	GCTTACTTGT	ATCCCAATAA	GCAAGATTCT	120
TTAGTTGTGC	AAGCAGATGG	GCTTTATAGT	GAAATTCCTG	GGTTTTTCAT	TTCTGTTTTCT	180
AGCAAGATCT	TGAAAGGAAT	TGGTGAGCCT	TTAGCCAATG	TTATCCAACC	TTTTGGTATG	240
GTTTTAGGAA	TGCTTTTAAT	CCTTTTGTAT	TCCTTTAAAC	GCTATCAAAA	CAATGATTTA	300
TTTGAAATCA	AAACCTTTTT	AATGCTTTTT	GTGTTTGTAG	GATACCTTTC	TTTGTACCAT	360
TATGCTTTTA	AATCTGATGG	TTCTAGTAGC	GGTAATGGTC	GCTCCAGTTT	TGCCTTTCAA	420
AATCATGTAA	CAGAAATTTT	TGACACGCCT	GCTAACTTGC	TAAATGCTGG	GATTTCTAAT	480
GTGGTTAAGG	AATATCAAAC	AAATAGTGCA	AGAGAACACA	AGAATATAGA	CACGCACCAC	540
AGTATCACTA	ACGCTAATAT	TTCAATCCAT	GTCAGACAAA	TTTTAACGAG	TTTGAATAAA	600
CTATATGAAG	ACTTCAAAAT	TAATAATGGA	CTATCGCTAA	AAACCCTTAT	TGCAGCTGTT	660
TTGTTATTAG	TTATTTTAGG	ATTAGAATTG	TTTTTATTGT	TCAAAGTTTT	CTGTTATGTT	720

978

TTTATGACTT	ATTTAGAAAA	AATTATTTAC	TTGTCTTTGG	TTATTTTCAT	GCTACTGCTA	780
GGGTTTTTTC	AGCAGACTAG	AGGTTTTTTA	GTGTCTTATG	TGAAAAAAT	TATTTTCATTG	840
ACTTTTTTACA	TGCCTTTTGT	GTGTCTATTA	GTGTATTTC	ACTCTTTTGC	ATTACAATAC	900
GCAATCAAAG	TGGGAGGGAG	CAATGAAATA	GTGGCTAAAT	TTGGCATTAT	TGTAGCAATA	960
GGAATTCAC	TGACATTAT	TCAAAAAGTC	CCCGAAATGA	TTAACGCTAT	CTTTGGCACA	1020
CAAGGTGGTC	TAACGGATGC	TAAAAGCTTC	ATATATCAAG	GTGTGCAAAT	GGCTAGTGCT	1080
GGAGCTGGAG	CCATAGCTGG	AAGTCTTAAG	AGTGTGGGTC	GTTTCAGCATT	TGGTAGAACG	1140
CTAGAAGCTT	ATAAAGACGC	AAAATCTACG	ATAAACAGCA	CTACGGCTAA	CATGAGAGAC	1200
ATGCCAGGAC	ATCCTGGTGT	TAGAGTGGGT	GTGGAGACGA	TTGAACCTCC	CAAGTCTCAT	1260
AGAGCTAGCA	AA					1272

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391

AAAAATCGCT	ATCTTAAGAG	GGGGCGAAAC	GCTATCTTGG	AACCTTCAAG	AAATCGCCTA	60
AAACATGCCG	CCTTTTTTGT	GGGGCTTTTT	ATCGTTTTGT	TTTTAATTAT	AATGAAGCAC	120
CAAACCTCCC	CCTATGCTTT	CACGCATAAT	CAAGCCCTTG	TCACTCAAAC	CCCCCCCCTAT	180
TTACGCGAAC	TCACTATCCC	TAAACCAAAT	GACGCTTTAA	GCGCGCATGC	GAGCTCTTTA	240
ATCAGCTTGC	CTAACGACAA	TCTTTTGAGC	GCTTATTTTA	GCGGCACTAA	AGAAGGGGCA	300
AGGGATGTGA	AAATCAGCGC	GAATCTTTTT	GACAGCAAGA	CTAATCGCTG	GAGCGAAGCC	360
TTCATTTCTT	TAACCAAAGA	AGAGCTTTCT	CATCATTCGC	ATGAATACAT	CAAAAAATTA	420
GGTAACCCCT	TGCTTTTTTT	GCATGATAAT	AAAATTTTGT	TGTTTGTCGT	AGGGGTGAGC	480
ATGGGCGGGT	GGGCCACTTC	TAAAACTAT	CAATTGAAA	GCGCTTTAGA	GCCGATTCAT	540
TTTAAGTTTG	CGCGAAACT	CTCTTTAAGC	CCTTTTTTAA	ATTTGAGCCA	TTTAGTAAGG	600
AATAAGCCTT	TAAACACCAC	TGATGGCGGG	TTTATGCTAC	CACTCTATCA	CGAATTAGCC	660
ACCCAATACC	CCTTGTTGTT	GAAATTTGAC	CAACAAAATA	ACCCAAGAGA	GCTTTTAAGG	720
CCTAATACCT	TAAACCACCA	GCTCCAACCA	AGCTTAACCC	CCTTTAAAGA	CTGCGCTGTC	780
ATGGCGTTTA	GAAACCATT	TTTAAAGAT	AGCCTCATGC	TAGAAACCTG	TAAAACCCCC	840
ACTGATTGGC	AAAAACCCAT	TTCTACAAAT	CTTAAAAACT	TAGATGATT	TTTAAATTTA	900
CTCAATTTAA	ATGGAATATT	GTATTTGATC	CACAACCCTA	GCGATTTATC	ACTGCGTCGT	960
AAAGAACTTT	GGCTTTCTAA	ATTAGAAAAC	TCCAACCTCGT	TTAAAACCTT	AAAAGTTTTG	1020
GATAAAGCGA	ATGAAGTGAG	TTACCCAAGC	TATAGCCTTA	ATCCGCATTT	TATAGATATT	1080
GTCTATACTT	ACAACCGCTC	TCATATCAAA	CACATCCGTT	TCAATATGGC	TTATTTAAAT	1140
TCCCTTCTCA	AG					1152

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

979

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...555
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392

TTAGTCATGT	TTATATCTTC	TTCTTACACG	CTGAGTTTTG	TATGGCTTTT	TTTAATTTTC	60
TTTTTTTTCA	AAAATAAGCC	ATTGGGTTTG	AGGTTTTTCG	TCTCTTTGAT	AAGCGTGATT	120
TTAAGCAATA	TCGCTTTGAA	AGACTCCCTA	TCGCTCAATG	AATTTTTAAG	CAGTTTTTACA	180
GCCCCCTTAA	GCCCCCTTAG	CTGTCTTTTG	ATCCTTGCTT	ATGCAAGCTT	TTCTTGCCAT	240
ATACTCAAAA	AGCCCCCTTT	AGAAACCTTG	CAATCTTATA	GCGTCATGCT	GTTTTTCAAT	300
CTGTTGCTTT	TGACAGATAT	TTTAGGGTTT	TTGCCTTTTT	CAATCTACCA	TCATTTTCATG	360
GCTTCTCTGA	TTTTTAGCGC	GCTTTTTTGC	AGCAGTTTGT	TTTTGAGTAG	CCCCTTATTA	420
GGCGTGATCG	CTTTAGTGGC	TTTATCCAGT	TCGCTTTTGA	TGCGTTCTAA	TTTTCAAATC	480
TTAGATTCTT	TATTGGATTT	CCCATTATTT	CTTTTGTCT	TTTTTAAGAC	TTTATATCTT	540
GCTAAAAAAA	GGTTA					555

(2) INFORMATION FOR SEQ ID NO:1393:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2946
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393

AAAAGAATAC	TGATGAAGAA	AAGAAAACAT	GTATCCAAGA	AAGTGTTTAA	TGTCATTATC	60
TTGTTTGTGG	CAGTATTCAC	TCTTTTAGTC	GTCATTCACA	AAACCCCTTC	AAACGGCATT	120
CACATACAAA	ATTTAAAAAT	TGGAAAACTT	GGCATTTCCTG	AATTATACTT	AAAACCTCAAT	180
AACAAGCTTT	CTTTGGAAGT	TGAGCGGGTT	GATCTCTCTT	CTTCTCTCCA	TCAAAAACCC	240
ACTAAAAAGC	GTTTAGAAGT	TTCTGATTTG	ATTAAAAATA	TCCGTTATGG	CATTTGCGCG	300
GTGCTTTATT	TTGAAAAACT	TAAAGTCAAA	GAAATCATTT	TAGACGATAA	AAATAAGGCC	360
AATATCTTTT	TTGATGGGAA	TAAATACGAG	TTAGAATTTT	CAGGAATCAA	AGGGGAATTT	420
TCCCTAGAAG	ACGATAAAAA	TATCAAGCTT	AAAATCATCA	ATTGCTTTT	TAAAGATGTT	480
AAAGTCCAAG	TGGATGGCAA	CGCCCACTAT	TCACCCAAAG	CCAGGAAAAT	GGCGTTCAAT	540
TTGATTGTCA	AGCCCTTAGT	TGAACCCAGC	GCTGCAATTT	ATTGCAAGG	GCTAACCGAT	600
TTAAAAACCA	TAGAATTAAA	AATTAACACT	TCTCCAATGA	AAAGCCTAGC	GTTTTTAAAG	660
CCTCTTTTCC	AACGCCAATC	GCAAAAAAAT	TTAAAAACGT	GGATTTTTGA	CAAGATCCAA	720
TTTGCCAGCT	TTAAGATTGA	TAACGCTTTA	ATCAAGGCTA	ATTCACTCC	TAGCGAGTTT	780
ATCCCATCGC	TTTTGGAAAA	TTCTGTAGTT	AAAGCCACTT	TGATTAAGCC	TTCACTCGTT	840
TTTAATGATG	GCTTATCGCC	CATTAAAAATG	GATAAAACCG	AATTGATTTT	CAAAAACAAA	900

SUBSTITUTE SHEET (RULE 26)

980

CAGCTCCTCA	TACAGCCCCA	AAAAATCACT	TATGAAACCA	TGGAATTAAC	CGGCTCTTAC	960
GCCACTTTTT	CCAAATTTGTT	AGAAGCCCCCT	AAGTTGGAGG	TTTTTTTAAA	AACGACCCCT	1020
AATTATTATG	GCGATAGCAT	TAAGGATTTA	TTGAGCGCTT	ATAAAGTCGT	TTTACCTTTG	1080
GATAAAATCA	GCAATGCCATC	TAGCGCGGAT	TTGAAGCTCA	CTTTGCAATT	CTTAAAAAAC	1140
ACCGCCCCCT	TATTTAGCGT	TCAAGGCAGC	GTTAATTTGC	AAGAAGGCAC	TTTCTCGCTC	1200
TATAATATCC	CCCTTTACAC	GCAAAGCGCT	CAAATCAATT	TGGACATCGC	CCAAGAATAC	1260
CAATACATCT	ACATAGACAC	GATCCACACG	CGCTATGCAA	ACATGCTGGA	TTTAGACGCT	1320
AAAATCGCTT	TAGATTTAGG	TCAAAAAAAC	CTTCTTTTGG	ATTCTTTTAGT	CCATAAAATC	1380
CAAGTCAATA	CCAATAACAA	TATCAACATG	CGCTCTTATG	ATCCCAATAA	CACTCAAGAA	1440
GATCCGCAAA	CTAACTTTAC	TTTGGATCTA	AAAAGCTTGC	ATTCTATCAT	TCAAGAGGGT	1500
GAAAATTGAG	AAGTTTTTAG	AAGAAAAATC	ATAGACACCA	TTAAAGCCCA	AAGCGAAGAT	1560
AAATTCTACT	AAGATGTTTT	TTACGCCACA	GGAGACACTC	TCAAAAGCCT	GTCGTTGAGT	1620
TTTGATTTTT	CCAACCCCGA	TCACATACAA	TGGAGCGTGC	CACAACTCTT	ATTAGAAGGC	1680
GAAATTTAAG	ATAACGCCTA	TACTTTTAAG	ATCAAAGATT	TGAAAAAGAT	CAAGCCCTAT	1740
TCCCCCATTA	TGGACTATAT	TGCCCTAAAA	GACGGCTCTT	TAGAGGTTTC	TACGAGCGAT	1800
TTTGTCAATA	TTGATTTTTT	TGCTAAAGAT	TTGAAATCA	ACCTCCCCAT	TTATAGGAGC	1860
GATGGATCGC	ATTTTGATTC	TTTTTCTTTA	TTTGGCTCTA	TCAATAAAGA	TGAAATTTCT	1920
GTCATATCTC	CAAGCAAAAAG	CATATCCATA	AAAGTTAAGG	GGGATCAAAA	GGATATTACC	1980
CTTAATAACA	TTGATTTGAG	TATTGATGAT	TTCTTGGATA	GTAAAAATGCC	AGCTATTGCG	2040
GGATTATCTT	CAAAAGAACG	AAAAGAAAAG	CCTAGCTCTA	AAGAAATCCA	AGATGAAGAT	2100
GTTTTCAATTA	GCGCCAAACA	ACGCTATGAA	AAAGCCCACA	AAATTATCCC	CATCTCTACA	2160
CGCATCCATG	CTAAAGATGT	CGTGTGATC	TATAAAAAAA	TGCCTTTTCC	TTTAGAAAAT	2220
CTTGATATTG	TCGCTCAAGA	CGATAGGGTG	AAAATTGATG	GCAATTATAA	AAACGCCATG	2280
ATCATGGCGG	ATTTAGTGCA	TGGGGCTTTG	TATCTTAAGG	CTCATAATTT	TAGCGGGGAT	2340
TATATCAACA	CCATTCTTCA	AAAAGATTTT	GTAGAAGGAG	GCTTATTAC	GCTTATTGGG	2400
GCTCTTGAAG	ATCAGGTTTT	CAATGGCGAA	TTGAAATTCC	AAAACACAAG	CTTAAAGAAT	2460
TTCGCCCTCA	TGCAAAACAT	GGTCAATCTC	ATCAACACCA	TTCCCTCCCT	TATTGTCTTT	2520
AGAAACCCCTC	ATTTAGGGGC	TAATGGCTAT	CAAATCAAAA	CCGGCTCCGT	TGTGTTTGGG	2580
ATCACTAAAG	AATATTTAGG	GTTAGAAAAA	ATTGATCTTG	TCGGCAAAAC	GCTTGATATT	2640
GCTGGCAATG	GAATCATTGA	ATTAGACAAA	AACAAATTAG	ATTTAACTTT	AGAAGTTTCC	2700
ACTATCAAGG	CTTTGAGTAA	TGTCTTAAAT	AAAATCCCTA	TCGTGGGCTA	TCTCGTTTTA	2760
GGAAAAGGAG	GTAAATCAC	CACTAACGTG	AATGTCAAAG	GCACGTTGGA	TAAGCCTAAA	2820
ACCCAAGTAA	CTTTAGCGTC	AGATATTATC	CAAGCGCCTT	TTAAAATCTT	ACGCCGTATT	2880
TTACAGCCTTA	TTGACATCAT	CGTGGATGAA	GTCAAGAAAA	ACATTGATTC	AAAAAGGAAA	2940
TTAAAA						2946

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394

AGACCATTCA	GATCGCTTAT	AAGGATTACC	CACGCCCCAA	AACATAAAACC	CTCATTGCGA	60
TTAGAGTGCG	TTATTACTTG	GGAGGCAATT	AACAGCATGG	AAATCAGCCT	TTTTGACCCC	120
ATAGACGCCC	ACTTGCACTG	GCGAGAAAAC	GCGCTTTTAA	AAGCGGTGTT	GGAATATTCT	180
AGCGAACCTT	TTAGCGCCGC	AGTGATCATG	CCCAATCTCA	GTAAGCCTTT	GATTGACACT	240
CCAATCACCC	TAGAATATGA	AGAAGAAATT	TTAAAAAATT	CTTCAAACCT	CAAGCCTTTA	300

SUBSTITUTE SHEET (RULE 26)

981

ATGAGTTTGT	ATTTTAACGA	TGGTTTGACT	TTAGAAGAAT	TGCAACGAGC	TAAAAACAAA	360
GGCATTAAAT	TTTTAAAACT	CTACCCCAAA	GGCATGACCA	CAAACGCGCA	AAATGGCACT	420
TCCGATTGTG	TGGGTGAAAA	GACTTTGGAG	GTTTTAGAAA	ACGCCCAAAA	ATTAGGCTTT	480
ATTTTATGCC	TCCATGCAGA	ACAAGCTGGG	TTTTGTTTGG	ATAAAGAATT	TTTATGCCAT	540
AGCGTTTTAG	AAACTTTTCG	CCTTTCATT	CCTAAACTCA	AAATCATTAT	AGAGCATTG	600
AGCGATTGGC	GCAGTATCGC	TTTGATTGAA	AAGCATGACA	ACCTCTATGC	GACTTTGACC	660
TTACACCATA	TCAGCATGAC	TTTAGATGAC	TTATTAGGGG	GGAGTTTGGG	CCCGCATTTG	720
TTTTGCAAAAC	CCTTAATCAA	AACCAAAAAA	GACCAAGAAA	GGCTCTTATC	CCTTGCTTTA	780
AAAGCCCAAC	CTAAATCTC	TTTTGGATCG	GACAGTGCCC	CGCATTTTAT	TTCTAAAAAG	840
CATAGCGCTA	ACATCCCGGC	GGGCATCTTT	TCTGCCCCCTA	TTTTGTTGCC	TGCGTTGTGC	900
GAACTTTTTG	AAAAACACAA	CGCTTTAGAA	AAATTGCAAG	CCTTTATCAG	TGATAACGCT	960
AAAAAATCT	ACGCGCTAGA	CAATTTACCC	AGTAAAAAAG	CGCATTTGTC	TAAAAAACCC	1020
TTTATAGTCC	CTACGCACAC	GCTTTGCTTG	AATGAAAAAA	TCGCTATCTT	AAGAGGGGGC	1080
GAAACGCTAT	CTTGGAACT	TCAAGAAATC	GCC			1113

(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395

GAAATTTTATA	TGCCGGAAAA	TTCTAAACTA	CAACCTGCTA	AGTTAGGGAA	AAATTTTGAC	60
CCTGTGGATC	ATTCTAACAG	GAATTTTTC	TTTTCTCTCA	TCTGTCTGT	ATTGTTACAC	120
TGGTTGATTT	ATTTTTTATT	TGAACACAGA	GAAGATTTTT	TTCCCTTCAA	ACCCAAGCTC	180
GTTAAATTA	ATCCTGAAAA	TTTATTTGGT	TTAAAAAGAG	GCCATTTCACA	AGATCCCAGT	240
AAAAACAACC	CAGGCGCTCC	TAAACCCACG	CTAGCTGGCC	CTCAAAAACC	CCCCACACCC	300
CCCACACCCC	CCACTCCGCC	AACCCACCA	AAACCTATAG	AAAAGCCAAA	GCCTGAGCCT	360
AAACCAAGC	CCTAACCCAGA	ACCCAAAAAG	CCCAACCACA	AACATAAGGC	GCTCAAAAAA	420
GTGGAAAAAG	TGGAAGAGAA	AAAAGTAGTA	GAGGAGAAAA	AAGAAGAGAA	AAAAGTAGTA	480
GAACAAAAAG	TAGAGCAGAA	AAAAATAGAA	GAGAAAAAAC	CTGTCAAAAA	AGAATTTGAC	540
CCTAACCAGC	TTTCTTTCTT	GCCTAAAGAA	GTTGCGCCAC	CCAGACAGGA	AAACAATAAA	600
GGCTTGGATA	ACCAGACTAG	AAGGGATATT	GATGAATTGT	ATGGCGAAGA	ATTGAGAGAT	660
TTAGGCACAG	CCCGAAAAAG	ATTTTCATCAG	GAA			693

(2) INFORMATION FOR SEQ ID NO:1396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

982

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396

AGTCGTTATC	ACCCAAGAGG	TTTGTAGCCAA	TTGCCTAAAC	TCAAACATCAT	TTGCATCACC	60
GCTACAGGCA	CGGATAATGT	GGATATAAAA	AGCGCGAAAG	CTTTAGGCAT	AGAAGTCAAA	120
AACGTGAGCG	CTTATTCTAC	CGAATCTGTA	GCCCAGCACA	CTTTAGCGTG	CGCGTTGTCT	180
TTGTTGGGGA	GGATCAATGA	TTACGATCGT	TATTGCAAAA	GCGGGGAATA	TAGTCAAAGC	240
GATATTTTTA	CGCACATTAG	CGATATTAAA	ATGGGGCTTA	TTAAAGGAGG	TCAATGGGGG	300
GTTATTTGGT	TAGGCAATAT	CGGTAAAAGA	GTCCGCAAGC	TCGCTCAAGC	TITCGGGGCA	360
AAGGTGGTGT	ATTTTTCCTC	TAAAGATAAA	AAAGAAGAAT	ACGAGCGCTT	GAGTTTAGAG	420
GAATTGCTTA	AAACAAGCGG	TATTATCAGC	ATTCATGCCC	CCTTAAATGA	AAGCACGCGC	480
GATTTAATCG	CTCTGAAAGA	ATTGCAAAGC	TTAAAGATG	GGGCGATTTT	AATCAATGTG	540
GGGCGTGGGG	GCATTGTGAA	TGAAAAGGAT	TTGCTTTTAA	TTTTAGAAAC	CAAAGATTTG	600
TATTACGCGA	GCGATGTG					618

(2) INFORMATION FOR SEQ ID NO:1397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397

ATATTAGAGA	ATTGTAGGAT	TTACGCCAGG	CTTTTGAAA	TGATACTAAA	AAATTGTGATT	60
TTGTTATTTT	TAGCAAAGAG	AAAACCTTAT	TTCATAGAAG	CTAATTTTTA	TACCATTAGT	120
GGGAGCAAGC	TTAATGAAGT	CGCAAGATCC	TATCAAGACT	TAGCTTTTAA	ATTGGAAGCA	180
TTTCTTAATT	ACGAATTIAT	TTGGATAACT	GATGGCATAG	GTTGGCTAGA	CGCTAAAAGC	240
AAGCTCCAAG	AAGCTTACAA	ATCTGTAGAA	ATCTATAACT	TAAGCTATGT	GAATGATTTT	300
ATATCAAAGG	TGCAAAAA					318

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398

TGCGTGATGC	TAATGGCAAT	TTTTACCCCT	TATATTCTTA	TTTTGAAAAT	GATGAAAAAG	60
TCTATGAGTT	TATTCGCCAA	TATGGGGTTG	GAGCAAATTT	TTTGCAACAG	AGACATTAAA	120
GATTTAATG	ATTTTGTTTT	TGGTATAGAA	GTGGGGCTTG	ATAGCAATGC	GAGAAAAAAT	180
CGTAGCAGAA	AGGCTATGGA	AAATCATCTT	ATCGGTCTTT	TTGTCCAAGC	TCAATTAAAT	240
TTTAAAGAAC	AAGTAGATAT	TAGAGAAATT	GAGGATTTAC	GCCAGGCTTT	TGGAAATGAT	300
ACTAAAAAAT	TTGATTTTGT	TATTTTTCAG	AAAGAGAAAA	CTTATTTTCA	TAGAAGC	357

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399

CTTGTGATCA	ATTCTAAAAC	CGGACTGCTC	ACCATTAAAG	GCGAGGACGC	TTTAGGCAAG	60
GCTAGTTTGA	AGGATTTGGG	TTTGAGCGCT	GGCATGGTGC	AATCTTATGA	AGCTTCGCAA	120
GACACGCTTT	TTATGTCTAA	GAATTTGCAA	AAAGCGAGCG	ATTTCGAATT	CACTTACAAT	180
GGGGTGAGCA	TCACGCGCCC	CACTAATGAG	GTCAATGATG	TGATCAGCGG	GGTTAATATC	240
ACTTTAGAGC	AAACCACAGA	GCCTAATAAG	CCTGCCATTA	TCAGCGTGAG	CAGAGACAAT	300
CAAGCCATTA	TAGACAGCCT	TAAAGAATTT	GTCAAAGCCT	ATAATGAGCT	TATCCCTAAA	360
CTAGACGAAG	ACACGCGCTA	TGACGCTGAC	ACTAAAATCG	CCGGGATTTT	TAACGGCGTG	420
GGCGATATTC	GTGCCATTAG	ATCCTCTCTT	AATAATGTGT	TTTCTTATAG	CGTGCATACG	480
GATAATGGGG	TAGAAAGCTT	GATGAAATAC	GGGCTTAGTT	TAGACGATAA	GGGCGTGATG	540
AGTTTGATG	AAGCTAAATT	ATCAAGTGCA	TTAAATTCTA	ACCCTAAAGC	GACTCAAGAT	600
TTTTTCTATG	GGAGCGATAG	CAAGGATATG	GGGGGCAGAG	AAATCCACCA	AGAGGGCATT	660
TTTTCTAAAT	TCAATCAAGT	CATCGCTAAC	CTCATAGATG	GAGGGAACGC	TAAATTAAAG	720
ATTATGAAAG	ATTCCCTAGA	CAGAGACGCT	AAAAGCCTGA	CCAAAGACAA	AGAAAACGCT	780
CAAGAGCTTT	TAAAAACCCG	CTATAACATC	ATGGCGGAGC	GCTTTGCCGC	TTATGATAGT	840
CAAATCTCTA	AAGCCAATCA	AAAATTCAT	TCCGTGCAAA	TGATGATCGA	TCAAGCAGCG	900
GCTAAAAAGA	AT					912

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

984

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...387
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400

AGGAACATTA TGCAATACGC TAACGCTTAT CAAGCCTACC AGCATAACCG AGTGAGTGTG	60
GAATCCCCCG CAAAACTCAT TGAATGCTT TATGAAGGGA TTTTAAGATT TTCTTCGCAA	120
GCCAAACGCT GTATTGAGAA TGAAGACATT GAAAAGAAGA TCTATTATAT TAATAGGGTT	180
ACGGATATTT TCACGGAGTT GTTGAATATT TTAGACTATG AAAAAGGGGG GAAAGTGGCG	240
GTGTATCTTA CAGGCTTATA CACCCATCAA ATCAAAGTTT TAACGCAAGC CAATGTGGAA	300
AATGACGCGA GTAAGATTGA TTTGGTGTTG AATGTGGCTA GGGGGTTGTT AGAGGCATGG	360
AGGGAAATCC ATTCAGATGA ACTCGCC	387

(2) INFORMATION FOR SEQ ID NO:1401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401

TTTGATGATC TTTATGGATC AAACCTCACTT CCATTTTATC CACGGGTAAC CCCGGTAAAA	60
TTCCCCACTT TCAAATGGGC GTTACTCAA GCGTTGATTA AGGACGATTT CCCCACATTA	120
GGCTGGCCCA CAAGGGCGAC AATGATTTCT TTCAATTGGT TTGAATGCTC CGCATTAAAA	180
GTTTTTTTAA TTTTGGTTA TATAGTTTTT AAAAGTTGGC ACTATAGCGC TATAAGACTA	240
ATTGTTATA	249

(2) INFORMATION FOR SEQ ID NO:1402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

985

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402

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AAGCGAGACA AGAATGTTAA AATGCGAAAG GGGCGTGTGA TGTATGCGT GTTTGATATA      60
GAAACCATTC CTAATATAAG CTTGTGTAAA GAGCATTTTC AATTAAAAGA AGACGATGCG      120
CTAAAAATCT GTGAATGGAG TTTTGAAAAG CAAAAAGAAA AAAGCGGGAG CGAGTTTTTG      180
CCCCTTTTAT TGCAATGAAAT CATCTCTATT GCAGCAGTCA TTGGCGATGA TTACGGGCAA      240
TTTATCAAAAG TAGGGAATTT TGGTCAAAAA CACGAGAATA AAGAGGATTT TCGAGCGGAA      300
AAAGAGCTTT TAGAGGACTT TTTCAAATAC TTTAACGAAA AGCAACCGCG CCTAATAAGC      360
TTTAATGGCA GAGGTTTTGA TATTCCCTTA CTCACGCTCA AAGCCCTTAA ATACAATTTA      420
ACCTTAGACG CTTTTTACAG CCAAGAAAAC AAATGGGAAA ATTACCGCGC GCGTTATAGC      480
GAGCAGTTTC ATTTGGATTT GATGGATAGC TTGAGCCATT ATGGATCCGT TAGGGGGTTG      540
AATCTAAATG GCGTTTGCTC TATGACGAAT ATTCTTGGTA AATTGATGT GAGCGGGGAC      600
TTAGTGCATG CGATTTATTA CAACCCCAT TTAAGGCCAA AAGGAGGAAA AAGGCATTAT      660

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(2) INFORMATION FOR SEQ ID NO:1403:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...762
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403

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AGATTTAAGG CTAGAATGT GCGTTTTTTC ATTTTTTTAA TTCTCATTTG CCCTTTAATA      60
TGCCCCCTAA TGAGCGCGGA TAGCGCTTTA CCTAGCGTCA ATCTCTCTTT AAACGCTCCT      120
AGTGATCCTA AACAACTCGT AACCAACCCTT AATGTCATCG CCTTACTCAC GCTTTTGGTT      180
TTAGCCCCAT CGTTGATTTT AGTGATGACG AGTTTCACCC GTTTGATCGT GGTGTTTTCT      240
TTTTTAAGGA CCGCTTTAGG CACGCAACAA ACCCCACCCA CTCAAATTCT AGTCTCGCTC      300
TCTTTGATAT TGACTTTTTT TATCATGGAA CCTAGCTTGA AAAAGGCTTA TGATACAGGG      360
ATTAAGCCTT ATATGGATAA AAAGATTTCT TACACCGAAG CGTTTGAAAA AAGCACTCTG      420
CCTTTCAAGG AATTCATGCT TAAAAACACA CGAGAAAAAG ATCTAGCCCT TTTTTTTAGG      480
ATTAGGAATT TGCCTAACCC TAAACCCCT GATGATGTGA GCTTGAGCGT TTTAATCCCG      540
GCATTATGA TAAGCGAGTT GAAAACAGCG TTTCAAATCG GCTTTTTACT CTACTGCCT      600
TTTTTGGTGA TTGATATGGT TATCAGCTCT ATTTTAATGG CGATGGGTAT GATGATGCTC      660
CCGCCTGTAA TGATTTCTCT GCCTTTTTAA ATTTTGGTGT TTATTCTGGT GGATGGGTTT      720

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SUBSTITUTE SHEET (RULE 26)

986

AATTTATTGA CCGAAAATTT AGTGGCGAGT TTTAAAATGG TT

762

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404

AAGTGGGGAA	TTTTACCGGG	GTTACCCGTG	GATAAAATGG	AAGTGAGTTT	GATCCATAAA	60
GATCATCAAA	TCACTATCAT	TGATTTACCG	GGCACTTACG	CGCTCAATGA	CTTCACCACT	120
GAAGAAAAGG	TGACTAAAGA	TTTTTTAGAA	AAAGGGCAAT	ACAATCTCAT	TCTCAATGTG	180
GTGGATTCCA	CCAAATTTAGA	GCGTAATTTA	GCCTTAAGCG	CGCAGTTATT	AGACACAAAT	240
AAAAAATGCT	TGCTTGCGCT	CAACATGTGG	GATGAAGCCA	AGAAGAAGG	GATCAACATC	300
AATACAGAAA	AGCTCTCTCA	AGAATTGGGG	GTTGTGTGCG	TGCCAACAAG	CGCGAGATCC	360
AAAGAAGATC	GCTTGAACAC	AGAGCTTTTA	TTAGACGAAA	TTGTCAAGCT	TTATTCTCAA	420
AACACTACAA	ACAACGAAAA	CATCAAAGTC	CCATCTCAAA	GTTTTAAAGA	GTCTTTAAAA	480
TACAGCCAGA	GCGCCCAAAG	AATCGCTAAA	TCAGTGATCA	GTGAAAACAA	ACAAAAATGCG	540
AGTTTTGAAC	ACACTTATAA	GATTGATAAG	ATTTTAATGC	ACCAGCGTTA	TGGGATTTTC	600
ATTTTTTTAG	GGTTTATGTT	TATCATCTTT	TCTTTGAGCT	TTTTAATAGG	AGGGGGAGTG	660
CAAAAAGCCC	TTGAAGAAGG	GTTTAAATTT	TTGAGCGATA	GTATTAAAGA	AAATGTGGCT	720
AATGAAGATT	TAGCGTCTTT	GGTGGGCGAT	GGCATTATTG	GGGGAGTGGG	AGCGACGGTT	780
TCATTCTTGC	CTTTAATTGT	GGTGTGTAT	TTTGGGATTT	CTTTACTAGA	GACGACAGGC	840
TATATGAGTA	GGGTAGCGTT	TTTACTAGAC	GGGATCTTGC	ATAAATTTGG	TTTGCATGGG	900
AAGAGTTTTA	TCCCTTTAAT	CACCGGTTTT	GGTTGCTCAG	TGCCTGCTTA	CATGGCGACA	960
AGAACCTTAC	AAAACATATA	CGAACGATTG	ATCACGCTTT	TTGTGATCGG	CTTTATGAGT	1020
TGCTCGGCAA	GACTGCCTAT	TTATGTGCTG	TTTGTAGGCT	CGTTTTTCCC	CTCTTCAAGT	1080
GCTGGGTTTG	TGCTGTTTTG	CATTTATATT	TTGGGGGCGG	TTGTGGCGTT	AGTGATGGCC	1140
AAATTACTCA	AAITTAAGCGT	GTTTAAAGGA	CAGACTGAAT	CCTTTATCAT	GGAAATGCCC	1200
AAATACCGCT	TTCCCAAGTTG	GAGAATGGTC	TATTTTCAGTA	TTTACACCAA	ATCGCTTTCT	1260
TACCTCAAAA	AAGCCGGGAC	TTATATTTTA	GTGGGAGCGA	TTTTGATCTG	GTTTATGTCC	1320
CAATACCCCTA	AAAATGATGC	GGCTATGAAG	ACTTATAAAC	AAGAAAGCTT	GTTAGTCCAA	1380
AAAAACGCTA	ATCTTTCAAG	CGAAGCTAAA	GAAGAAAAAT	TAAAAGAATT	AAAAACCGAA	1440
TTGGATAAAA	AGAATTTAAA	AAATAGCGTT	GTAGGAAGAG	GCGGGGCGTA	TTTAGAAAAA	1500
GTCTTTAACC	CTATGGATTT	TGATTGGCGT	TTGAGCGTCT	CGCTTGTAAC	CGGTTTTATG	1560
GCTAAAGAGG	TGGTGGTTTC	TACTTTGGGG	GTGTTGTTTT	CTTTAGGGGA	TCAAACGAA	1620
AAATCTGATG	CTTTTAGAGA	GATAATCAGA	AAAGAAGTCA	GCGTGCCCTAG	CGGGATCGCT	1680
TTTATCGTGT	TTGTGATGTT	TTATATCCCT	TGTTTTGCAG	CGACCATTAC	TTTTGGTAGG	1740
GAAGCTGGGG	GGATCAAGTT	TGTAGCGTAT	TTATTCATCT	TCACAACCGT	TGTAGCGTAT	1800
GCGTTTTTCCT	TGATAGCTTT	TTATGCGACT	CAAATTTTGG	TT		1842

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

987

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405

ATGAAAAGAA	TTTTAGTTTC	TTTGGCTGTT	TTGAGTCATA	GCGCGCATGC	TGTCAAAACT	60
CATAATTGG	AAAGGGTGG	AGCTTCAGGG	GTGGCTAACG	ATAAAGAAGC	GCCTTTAAGC	120
TGGAGGAGCA	AGGAAGTTAG	AAATTATATG	GGTTCTCGCA	CGGTGATTTC	TAACAAGCAA	180
CTCACTAAAA	GCGCCAATCA	AAGCATTGAA	GAAGCTTTGC	AAAATGTGCC	AGGCGTGCAT	240
ATTAGAAACT	CTACCGGTAT	TGGAGCTGTG	CCTAGCATTT	CCATTAGGGG	GTTTGGTGCT	300
GGAGGCCCCAG	GGCATTCTAA	TACGGGAATG	ATTCTAGTCA	ATGGGATTCC	TATTTATGTC	360
GCGCCCTAG	TTGAAATTGG	CACGGTTATT	TTTCCTGTAA	CCTTTCAGTC	TGTGGATAGA	420
ATCAGCGTAA	CTAAGGGTGG	GGAGAGCGTG	CGTTATGGCC	CTAACGCTTT	TGGCGGTGTG	480
ATCAACATCA	TCACCAAAGG	CATTCCTACC	AATTGGGAAA	GTCAGGTGAG	CGAGAGGACC	540
ACTTTTGGG	GCAAGTCTGA	AAACGGGGGC	TTTTTCAATC	AAAATTCTAA	AAACATTGAT	600
AAAAGCTTAG	TTAATAACAT	GCTTTTAAAC	ACCTATTTAA	GAACGGGGGG	TATGATGAAT	660
AAGCATTTTG	GAATCCAAGC	TCAAGTCAAT	TGGCTCAAAG	GGCAAGGGTT	TAGATACAA	720
AGCCCTACGG	ATATTCAAAA	TTACATGTTA	GATTCAATTG	ATCAAATCAA	TGATAGCAAT	780
AAAATCACCG	CTTTTTTTCA	ATATTATAGT	TATTTCTTGA	CAGACCCTGG	ATCTTTAGGC	840
ATAGCCGCTT	ACAATCAAAA	TCGTTTTCAA	AACAACCGCC	CCAATAACGA	TAAAAGCGGG	900
AGAGCGAAGC	GATGGGGAGC	TGTGTATCAA	AACTTTTTTG	GGGACACGGA	TAGGGTAGGG	960
GGGGGATTC	ACTTT					975

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2391 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406

AGACTAAAC	CAAATGTTAT	AGAGCGTAGG	ATGTTAGAAA	AGCTTTTAAG	CGCTATCAAA	60
CAAAAAGTTT	CAAACTATTT	TTTAGGGGTT	TTGCCTAAAA	GCTATTCTAT	GAGCGAAGAA	120
AACAACATTT	TAGGCTTGTA	TGATGAGCAT	TTTTTGCTCA	CTAAAAACGA	AAACTTAGTG	180
GGCATCTCC	GTTTAGAGGG	GGTTAGCTAC	ACCCATTTAA	GCACAGAGCA	ATTGCAAGAT	240
CTTTTCACTG	AGCGCCAAAT	GGCGTTAGAT	TCTTTAGAAA	AAGTCGTGGC	GCGTCTTGTC	300
GTTAAAGGC	GTAATTTGA	TTATAAACAA	AGCATTCAAT	CTGACTCTCA	ATACTTGCAA	360

SUBSTITUTE SHEET (RULE 26)

988

GCGATCTTGA	ATCAGTTTGA	AAATAAAGAA	GTGTATGAGA	ATCAGTATTT	TTTAGTTTGA	420
GAAAGCACTC	ACTCTTTTGA	TGGCGTTTGG	GAGCATAAGA	AAAAATCTTT	CATGCACGCT	480
AATAGAGAAA	ATTTTAAAGGA	TATTCTCTCT	TATAAAGCGC	ATTTTTTGA	AGAAACTTTA	540
AAAAGCTTAG	AAATCCAGCT	CAAAAACCTAT	GCCCCCAAAC	TCTTAAACTC	TAAAGAGGTT	600
TTGAATTTTT	ATGCAGAATA	TATTAATGGG	TTTGAACCTC	CTTTAAAACC	CCTAGTAGGG	660
GGGTATTTGA	GCGATAGCTA	TATCGCTAGT	TCTATCACTT	TTGAAAAAGA	TTATTTTCATT	720
CAAGAAAGCT	TTAATCAAAA	AACCTATAAC	CGCTTGATTG	GCATTAAAGC	TTATGAGAGC	780
GAAAGGATCA	CTTCTATAGC	GGTGGGAGCG	CTTTTATACC	AAGAGACGCC	TTTGATATTT	840
ATCTTTTCCA	TAGAGCCTAT	GAGCGTCAAT	AAAACGCTGA	GTTTTTTAAA	AGAGAGGGCC	900
AAGTTTAGCA	TGTCTAATCT	TGTTAAAAAC	GAGCTATTAG	AATACCAAGA	ATTAGTCAAA	960
ACCAAACGAT	TATCCATGCA	AAAATTCGCC	CTAAACGTTT	TTATCAAAGC	CCCCAGTTTG	1020
GAGGATTTAG	ACGCTCAAAC	CAGCTTAATT	TTAGGGCTTT	TATTTAAAGA	AAACTTAGTG	1080
GGCGTTATAG	AAACTTTTGG	CTTGAAAGGG	GGGTATTTTT	CCTTTTCCCC	TGAACGCATC	1140
CATTTAAACC	ACCGCTTGCG	TTTTTTAACC	TCTAAAGCCC	TAGCGTGTGT	GATGGTGTGT	1200
GAAAGGCAAA	ATTTAGGTTT	TAAGGCTAAT	TCATGGGGGA	ATAGCCCTTT	GAGCGTGTGT	1260
AAAAATTGGG	ATTATTCCCC	TTTTTTATTTC	AATTTCCACA	ACCAAGAAGT	GAGCCATAAT	1320
AACGCTAAAG	AAATTGCCAG	AGTGAATGGG	CATACTTTAG	TTATAGGGGC	AAACCGGAAGC	1380
GGTAAAAGCA	CGCTGATTAG	CTATTTAATG	ATGAGCGCTT	TAAAATACCA	AAACATGCGC	1440
CTTTTAGCTT	TTGACAGGAT	GCAAGGGTTG	TATTCCTTCA	CCGAATTTTT	TAAAGGGCAT	1500
TACCATGACG	GCCAATCTTT	TAGTATCAAC	CCCTTTTGTT	TAGAGCCTAA	TTTGCAGAAAT	1560
TTAGAATTTT	TGCAATCCTT	TTTTTTGAGC	ATGTTGGATC	TTGCCCTTTC	AAGGGATAAA	1620
GAAGCCTTAG	AAGACATGAA	TGCGATTTCT	GGCGCGATTA	AGAGCCTTTA	TGAGACCTTA	1680
TACCCCAAAG	ATTTTAGTTT	GCTGGATTTT	AAAGAAACGC	TTAAAAGAAC	CTCATCTAAC	1740
CAATTGGGCT	TGAGTTTAGA	GCCGTATTTG	AATAACCCCC	TTTTTAACGC	TTTGAATGAC	1800
GCGTTCAACT	CCAACGCTTT	TTTAAATGTG	ATAAACCTAG	ATGCGATCAC	CCAAAACCTT	1860
AAAGACTTAG	GGCTTTTAGC	CTATTACTTG	TTTTATAAGA	TCTTAGAAGA	GTCTAGGAAA	1920
AACGACAGCG	GCTTTTGGT	TTTTTTAGAC	GAATTTAAAT	CCTATGTGGA	AAACGATTTG	1980
TTAAACACTA	AAATCAACGC	TTTAATCACG	CAAGCCAGGA	AAGCTAATGG	CGTGGTGGTG	2040
TTGGCCTTGC	AAGACATTTA	CCAACCTAGC	GGGGTTAAAA	ACGCCCATAG	TTTTTTAAGC	2100
AACATGGGGA	CTCTCATTTT	GTATCCGCAA	AAAAACGCTA	GGGAATTGAA	ACACAATTTT	2160
AATGTGCCCT	TGAGCGAAAC	TGAAATTTCT	TTTTTAGAAA	ACACCCCTCT	GTATGCCAGG	2220
CAGGTTTTAG	TCAAAAATCT	GGGTAACGGG	AGTTCCAACA	TGATTGATGT	GAGTTTGGAG	2280
GGCTTGGGGT	GTTATTTGAA	AATCTTTAAT	TCAGATTCCA	GTCATGTCAA	TAAAGTGAAA	2340
GCCTTACAAA	AAGACTACCC	TACAGAGTGG	CGTGAGAAAC	TTTTGAAGAG	T	2391

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407

AAAATGATTC	TTAAAAGTTC	CATTGATCGC	CTTTTACAAA	CGATAGATAT	TGTAGAAGTC	60
ATTAGCTCTT	ATGTGGATT	GAGGAAATCA	GGTTCGAATT	ACATGGCTTG	TTGCCCTTTT	120
CATGAAGAAA	GGAGCGCGAG	TTTTAGCGTC	AATCAAGTTA	AAGGGTTTGA	CTATTGCTTT	180
GGGTGTGGGG	CGAGCGGGGA	TAGCATTAATA	TTTGTGATGG	CGTTTGAAAA	ACTTTCGTTT	240
GTGGAAGCGC	TTGAGAAATT	AGCCCAACGA	TTCAATATAG	CTTTAGAGTA	TGACAAAGGC	300
GTTTATTACG	ATCATAAAGA	AGATTACCAC	CTTTTAGAAA	TGGTGAGTTC	GTTGTATCAA	360

SUBSTITUTE SHEET (RULE 26)

GAAGAGCTTT	TTAACGCCCC	GTTTTTTTGG	AATTATTTGC	AAAAAAGAGG	GCTTAGCATG	420
GAGAGCATCA	AAGCGTTTAA	GTTAGGCTTA	TGCACGAATA	AAATTGATTA	CGGCATGAA	480
AATAAAGGCT	TGAATAAGGA	CAAATTGATT	GAATTGGGCG	TGCTAGGCAA	GAGCGATAAA	540
GAGGATAAAA	CCTATTTGCG	CTTTTTGGAT	CGCATCATGT	TCCCTATTTA	TAGCCCTAGT	600
GCTCAAGTGG	TGGGTTTTGG	AGGGCGCACC	TTAAAAGAAA	AAGCGGCCAA	GTATATCAAT	660
TCGCCCCAAA	ATAAGCTTTT	TGATAAATCC	AGCTTGCTCT	ATGGCTATCA	TTTGGCTAAA	720
GAACACATT	ATAAACAAAA	GCAGGTCATT	GTAACAGAAG	GGTATTTGGA	TGTGATTTTA	780
TTGCACCAGG	CGGGTTTTAA	AAACGCCATA	GCCACGCTTG	GGACAGCTTT	AACGCCATCG	840
CATTTGCCCT	TGCTTAAAAA	AGGCGATCCA	GAAATCCTTT	TGAGCTATGA	TGGGGATAAG	900
GCAGGGCGGA	ATCGGCTTA	TAAAGCGAGC	TTGATGTTAG	CTAAAGAGCA	AAGGAAAGGG	960
GGGGTGATTT	TGTTTGA AAA	CAACCTAGAC	CCAGCGGATA	TGATCGCTAA	TCATCAGATT	1020
GAAACTTTAA	AAAATTGGCT	ATCGCGCCCC	ATAGCTTTCA	TTGAATTTGT	TTTAAGGCAC	1080
ATGGCGGGTT	CTTATCTTTT	AGACGATCCT	TTAGAAAAAG	ATAAGGCCCT	TAAAGAAATG	1140
TTAGGGTTTT	TGAAAAACTT	TTCCTTGCTT	TTACAAAATG	AATACAAGCC	CTTAATCGCT	1200
ACGCTTTTGC	AAGCGCCTTT	GCATGTTTTA	GGGATTAGAG	AGCCAGTTTC	TTTTTCAGCCT	1260
TTTTACCCCA	AAACAGAAAA	GCCTAATCGC	CCTCAAAAGT	TCGCGCATGT	TTCTAGCATG	1320
CCCAGTTTGG	AATTTTTTGA	AAAATTGGTG	ATCCGCTACC	TTTTAGAAGA	CAGAAGCCTA	1380
TTGGATTAG	CGGTGGGTTA	TATCCATAGT	GGGGTATTCT	TGCATAAAAA	ACAAGAATTT	1440
GACGCTTTAT	GTCAAGAAAA	ATTGGACGAC	CCTAAATTAG	TGCGGTTATT	ATTAGATGCG	1500
AATTTACCCC	TAAAAAAGG	GGGTTTTGAA	AAGGAATTGC	GTTTGTGAT	TTTGGCGTAC	1560
TTTGAGCCGC	CAACTCAAAG	AAATCCC				1587

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408

CTAAGAGGGC	ACAGGCGTAC	TTATATAGGC	TCCATGCCCG	GGCGTATTGT	CCAAGGGCTT	60
ATTGAAGCTA	AAAAGATGAA	TCCGGTCATG	GTTTTAGATG	AAATTGATAA	GGTGGATCGA	120
AGCGTTAGGG	GCGATCCAGC	GAGTGCTTTA	TTAGAGATCT	TAGACCCTGA	GCAAAATATC	180
GCCTTTAGGG	ATCATTACGC	GAATTTACGC	ATTGATTTGT	CGCAAGTGAT	TTTTATCGCT	240
ACCGCTAATA	ATATTGACAG	GATCCCAGCT	CCTTTAAGAG	ACAGAATGGA	ATTTATCAGC	300
GTGTCCAGCT	ACACGCCCTAG	CGAAAAAGAA	GAGATCGCTA	AAAACCTACCT	CATCCCCCAA	360
GAATTAGAAA	AGCACGCCCTT	AAAGCCTAGC	GAAGTGGATA	TTAGCCATGA	ATGTTTGAAA	420
CTCATTATTG	AAAAATACAC	CAGAGAAGCG	GGCGTTAGGG	ATTTACGAAG	ACAGATCGCA	480
ACGATTATGC	GTAAAGCGGC	TTTAAAATAC	CTAGAAGATA	ACCCGCACAA	AAAAGGGCGG	540
ACCAAAAAAA	GCGAAGACAA	AGATAAAAAA	GGCGGAAATG	AAGAAAAACGA	AAAAGAGAGT	600
GAGAGTAAAG	ATTTTTCGCT	CTCTATCACG	CCTGATAACC	TTAAAGAGTA	TTTAGAACCG	660
ATGGTGTTTG	AAATTGACCC	CATAGATGAA	GAAAAATAAA	TCGGTATCGT	CAATGGCTTG	720
GCATGGACTC	CAGTGGGCGG	TGATGTGCTT	AAAATTGAAG	CGGTTAAGAT	TAGAGGCAAG	780
GGGGAATTGA	AACTCACCGG	GAGTTTGGGC	GACGTGATGA	AAGAATCCGC	CATTATTGCC	840
TTTTCTGTTG	TCAAAGCTTT	GTTGGATAAC	GAAACCTTAA	AAGTGCCCTAA	AATCCCTAGC	900
GAGACCGATG	CAGAGAATAA	GAAAAAGAAA	AAAGTGCTGA	AAGTTTATAA	CGCTTACGAT	960
TTGCACCTGC	ATGTCCCTGA	GGGGGCTACG	CCTAAAGACG	GCCCGAGCGC	TGGGATCGCT	1020
ATGGCCGAGC	TGATGGCGAG	CATTTTGTGC	GATAGGGCTA	TAAGAAGCGA	AGTGGCGATG	1080
ACGGGCGAAT	TGACTTTGAG	CGGGGAAGTT	TTACCCATAG	GGGGGTGAA	AGAAAAATTG	1140

SUBSTITUTE SHEET (RULE 26)

990

ATCGCTGCTT	TTAAAGCCGG	CATCAAAACC	GCTCTCATT	CTGTCAAAA	TTACGAAAGG	1200
GATTTAGACG	AGATCCCTAC	TGAAGTCCGA	GAGAATTTAA	ACATCGTTGC	GGTGAAAAAC	1260
ATCGCTGAAG	TGTTAGAAA	AACCTTGCTT				1290

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409

AAAAGATATA	GAAAACTGC	TCTCTTACGG	CTTGACAATG	GCGACAAGCT	GTCATTAATG	60
AGGGAATTTT	TTAAAGCGT	TAGAGGGTTT	TTGAACCTTC	TTAGAATGAT	TTTCCCGGAG	120
CGCTTTCAAA	ACGCCTTTTT	AGGGTTAAGC	GAATTGTTTT	ACTACGCTTC	CAGCTTGAGT	180
TTTTATACGA	TTTTGTCTTT	ATCGCCTATT	TTGTGTTCG	TGTTCACTCT	TTTTGTGTCT	240
CATTACTTGC	AAGCGCACAG	CGGTGAAATG	GAAGCCTTGA	TTTTCCCTAA	CGCTCCTAAA	300
CTCATTGGCG	CGATTAAGGA	TTTTTTAGAA	AATTTTAAAA	AAACAGACAT	GACCTTAGGC	360
ACGCTTGAAG	AGGTGTCTAT	TGTGGTGGCG	TTGGTGCTTT	TTTGTGAAAA	CTACCGCTCC	420
ATCGCGTCAA	AAATTTTGA	CGCAAAGCCC	AGAGATTATG	CGCATTTTAA	GGGTAAAGAA	480
ATCTTTTAT	TTTGGGGGTT	TGGCAGGACT	TTAGTGTTTT	TATTCGCTTT	GCCTTTGGTG	540
GTGTTTTTTG	ATATTAGAT	CCAAGTGT	TTTGAAGATA	AAGATTCAAG	CTTGTTCAT	600
GTTTTAAGAT	GGATAGGCAC	TTACGCGTTT	TTTTTGATCC	TTTTTACCAT	TCCCACGAAT	660
AAGGTGTTTA	AACATTATTT	TTGGGTGTTT	TTATGGGTGT	TTTTTACGAG	CGTTTCTTGG	720
CATGTGCTGA	AATGGGCTTC	CACCTTATTT	ATGTGTTATA	CCAATCCGCA	CTTACTCATG	780
AGCCTGTATG	GGAGCCGTTT	CCCATTTTGT	GGTTTT			816

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...747

991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410

GTAGGTGTTG	TTATGATAAA	AAAGACCCTT	GCATCGGTTT	TATTAGGATT	GAGTTTGATG	60
AGTGTGTTAA	ATGCCAAAGA	ATGCGTTTCG	CCCATAACAA	GAAGCGTTAA	GTATCATCAG	120
CAAAGTGCTG	AGATCAGAGC	CTTGCAATTA	CAAAGTTACA	AAATGGCGAA	AATGGCGCTA	180
GACAATAACC	TTAAGCTCGT	TAAAGACAAA	AAGCCAGCCG	TCATCTTGGA	TTTAGATGAA	240
ACCGTTTTGA	ACACTTTTGA	TTATGCGGGC	TATTTAGTCA	AAACTGCGAT	TAAATACACC	300
CCAGAACTT	GGGATAAATT	TGAAAAAGAA	GGCTCTCTTA	CGCTCATTCC	TGGAGCGCTA	360
GACTTTTTAG	AATACGCTAA	TTCTAAGGGC	GTTAAGATTT	TTTACATTTC	TAACCGCACC	420
CAAAAAATA	AGGCATTAC	TTTAAAAACG	CTCAAAAGCT	TTAAGCTCCC	CCAAGTAGT	480
GAAGAATCCG	TTTTGTAA	GGAAAAAGGC	AAGCCTAAG	CCGTTAGGCG	GGAGTTAGTC	540
GCTAAGGATT	ATGCGATTGT	TTTACAAGTG	GGCGACACTT	TGCATGATTT	TGACGCCATT	600
TTTGCTAAAG	ACGCTAAAAA	CAGCCAAGAA	CAACAAGCCA	AAGTCTTGCA	AAACGCTCAA	660
AAATTCGGCA	CAGAATGGAT	TATTTTACCC	AACTCTCTTT	ATGGCACATG	GGAAGATGGG	720
CCTATAAAG	CATGGCAAAA	TAAAAA				747

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411

CATGACAAA	AATTTGATCT	CTTAGGCGGA	GTCATGGATT	TCGTAGGGTT	TGAAGATTTA	60
AAATGCAAAG	ACAAAGAAAA	CTCTCAAAA	GTTTTTGTGA	TCCGTAACGA	TAAGTTAGGC	120
GATTTTTATT	TAGTGATTCC	CGCTTTAATC	GCTCTCAAGC	ATGCTTTTTT	AGAAAAAGGC	180
GTAGAAGTGT	ATTTGGGCGT	GGTTGTGCCT	AGCTATACCA	CCCCAATCGC	TTTAGAATTC	240
CCTTTCATTG	ATGAAGTTAT	CATAGAAGAC	AACCATTAG	CCACCACCCC	CAAAAACCGC	300
TCCACCGACG	CCCTTATCTT	TTTATTTTCT	AATTTTAAAA	ACGCCAAACT	TGCTTTCACT	360
TTGAGAAAAT	CCATCCCCTTA	TATCCTAGCC	CCAAAGACCA	AAATCTATTC	TTGGCTTTAT	420
CAAAAGAGAG	TGCGCCAAAA	CCGCTCTTTA	TGCTTAAAAA	CCGAATACGA	ATACAATTTG	480
GACTTAATCC	ATGCGTTTTG	TAAAGACTAC	GATCTCCCTA	ACGCTCAACT	TAAAAAATC	540
GCATGGAAGC	TTAAAGACAA	ATCCAAAGAG	CGATCCATCA	TCGCTTCAAA	ACTCAACGCT	600
AATGTTGATC	TATGTGGAT	TGGCGTGCAT	ATGCATAGCG	GAGGCAGTTC	GCCCGTATTG	660
CCCGCTTCGC	ATTTCAATTGA	GTTGATTGCA	ATCTTGCATG	AAAAATTAAG	TTGTGAGATC	720
ATTCTTATTT	GCGGGCCAGG	CGAGAGAAAA	GCCACAGAAG	AACTCCTTAA	AGAAGTCCCT	780
TTGCTCACC	TCTATGATAC	GAGCCATAGT	TTAGTGGATT	TAGCCAAATT	GTGCGCGAAT	840
TTAAGCGTCT	GTATCGGGAA	CGCTTCAGGC	CCTTTGCATG	TGAACGCTTT	ATTTGACAAC	900
CAATCTATCG	GGTTTACCC	TAACGAACTC	ACCGCCTCTA	TTGCCAGATG	GCGGCCTTTC	960
AACGAACAAT	TTTTAGGCAT	CACCCGCGCT	AATGGCTCAA	ACGATATGGG	TTTGATTGAC	1020
ATTCAAAAAG	AAAGCGAAAA	GATTATGGGA	TTTATCACAA	AAAATCTTTC	TCATCACATG	1080
CAAGAAAGA						1089

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1986 base pairs

SUBSTITUTE SHEET (RULE 26)

992

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412

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GGTAACACGA TTATAAAGAT GCAAAAATCA CTGATCACAA CCCCCATTTA TTATGTGAAT      60
GACATCCCTC ATATTGGCCA TGCTTATACG ACTTTGATTG CCGACACTTT AAAGAAGTAT      120
TACACGCTTC AAGGCGAAGA AGTCTTTTTT TTAACCGGCA CCGACGAGCA TGGGCAAAAG      180
ATCGAACAAA GTGCGAGACT GAGGAATCAA AGCCCCAAAG CTTACGCCGA TAGCATTAGC      240
GCGATTTTTA AAAACCAAGT GGATTTTTTC AATTAGATT ATGATGGTTT TATCCGCACC      300
ACAGACAGCG AGCATCAAAA ATGCGTGCAA AACGCCTTTG AAATCATGTT TGAAAAAGGG      360
GATATTTATA AAGGCACTTA TAGCGGGTAT TATTGCGTGA GCTGTGAGAG TTATTGCGCG      420
GTCTCTAAAG TGGATAATAC AGATAGTAAA GTCCTATGCC CTGATTGCTT GAGAGAGACC      480
ACGCTTTTGA AAGAAGAGAG TTATTTTTTC AAATGAGTG CGTATGAAAA GCCTTTATTG      540
GAGTTTTACG CTAAAAACCC TGAAGCGATT TTGCCCATTT ATCGTAAAAA CGAGGTAAC      600
TCTTTTATTG AGCAGGGTTT ATTGGATCTG TCTATCACGC GCACGAGCTT TGAATGGGGT      660
ATTCTTTTGC CTAAAAAGAT GAACGATCCT AAGCATGTGG TGTATGTTTG GCTGGACGCT      720
TTTGAACGCG CTAGGCATAT TGTGGGTAAG GATATTTTAC GCTTCCATGC CATTATTGG      840
CCAGCCTTTT TGATGAGTTT GAATTTGCCC TTATTCAAAC AGCTCTGTGT GCATGGGTGG      900
TGGACGATAG AGGGCGTGAA AATGAGTAAG AGCTTGGGTA ATGTTTTAGA CGCTCAAAAG      960
CTCGCCATGG AGTATGGGAT TGAAGAATTA CGCTATTTTT TATTGCGTGA GGTGCCTTTT      1020
GGGCAAGATG GGGATTTTTT TAAAAAGCG TTAGTAGAAC GGATTAATGC GAATTGAAT      1080
AAGGATTTGG GGAATTTGTT GAATCGTTTG CTAGGCATGG CTAAAAAGTA TTTCAATTAT      1140
TCTCTAAAAA GCACCAAAAT CACTGCGTAT TATCCTAAAG AGCTAGAAAA AGCACATCAA      1200
ATTTTAGATA ACGCTAATTC TTTTGTGCCT AAAATGCAAT TGCATAAGGC TTTAGAGGAA      1260
TTGTTTAATA TTTATGATTT TTTGAATAAA CTCATCGCTA AAGAAGAGCC GTGGGTCTTG      1320
CACAAAAACA ACGAATCAGA AAAATTAGAA GCCTTATTGA GTTTGATCGC AAACACGCTA      1380
CTACAATCAA GCTTCTTGCT CTATGCGTTC ATGCCAAAGA GCGCTATGAA ATTAGCGAGC      1440
GCTTTTCGTG TAGAATCAC GCCCAATAAT TACGAACGCT TTTTAAAGGC TAAAAAATTA      1500
CAAGATATGG TTTTACAAGA CACCGAGCCT TTATTTTCCA AAATTGAGAA AATTGAAAAG      1560
ATTGAAAAGA TTGAAAAGAT TGAAAAGATT GAAAAAGGGG AGGAAGCCCT AGCAGAAAAA      1620
GCAGAAAAAA AAGAAAAAGA AAAAGCCCCA CCAACACAAG AAAATTATAT TAGTATTGAG      1680
GATTTCAAGA AAGTAGAGAT TAAAGTGGGG CTATCAAAG AAGCTCAAAG GATTGAAAAA      1740
TCCAATAAAT TACTGCGCTT AAAAGTGGAT TTAGGCGAAA ATCGTTTGAG GCAGATCATC      1800
TCAGGGGATCG CTTTGGATTA TGAGCCTGAA AGCTTGGTGG GTCAAATGGT GTGCGTGGTG      1860
GCTAATTTAA AACCCGCAAA GCTTATGGGT GAAATGAGTG AGGGCATGAT TTTAGCGGTG      1920
CGAGATAATG ATAATCTGGC TTTAATCAGC CCTACCAGAG AAAAAATTGC AGGAAGTTTG      1980
ATCAGC                                     1986

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(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

993

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1026
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413

GGACGCATGA	TGAAATGT	AATAGACTTA	ATGGGGGCTG	ACCATGGGGT	TTTACCCATT	60
ATTGAGGGAG	TCTCAAGGGC	TTTAGAGAAT	AAGAGTTTTA	GCGTGGTTTT	AGTGGGGGAT	120
AAAGACAAAG	CGACCCCTTT	TATTTCTAAA	GAGTTAGCCA	GCAAAGTGGA	AATGATCCAC	180
ACGCAAGATT	ACATTAAAAT	GGAAGAAGCC	GCCACTGAGG	CGATTAGCG	TAAGGAATCT	240
TCCATTACT	TGGGCATGGA	TATTTTAAAA	AATGGGGCTG	ACGCTTTGAT	TTGAGCGGGG	300
CATAGCGGGG	CGACTATGGG	TTTAGCGACC	TTGCGTTTAG	GCGGTATCAA	GGGGTTGAA	360
AGGCCTGCTA	TTTGCACTTT	AATGCCTAGC	GTTGGCAAAC	GCCCTAGCGT	GCTATTAGAC	420
GCAGGAGCGA	ACACGGATTG	CAAGCCTGAA	TATTTGATTG	ATTTTGCTCT	CATGGGGTAT	480
GAATACGCTA	AAAGCGTGTT	GCATTATGAC	AGCCCTAAAG	TGGGTCTTTT	GAGTAATGGT	540
GAAGAAGATA	TTAAGGGGAA	TACGCTCGTT	AAAGAAACGC	ATAAAATGTT	GAAAGCTTAT	600
GACTTTTTTT	ATGGCAATGT	GGAGGGGAGC	GATATTTTCA	AAGGGGTTGT	GGATGTAGTG	660
GTTTGCGATG	GCTTTATGGG	GAATGTGGTC	TTAAAGACAA	CTGAAGGGGT	CGCTAGTGCG	720
ATAGGCTCTA	TTTTTAAAGA	TGAAATTAAA	AGCTCTTTTA	AATCTAAAAT	GGGGGCTTTG	780
ATGCTTAAGA	ACGCGTTTGG	TATTTTAAAA	CAAAAACCG	ATTACGCTGA	ATATGGGGGA	840
GCACCGCTTT	TGGGCGTGAA	TAAAAGCGTG	ATCATTAGCC	ATGGCAAGAG	CAACGCTAGA	900
GCGGTGAAT	GCGCGATTTA	TCAGGCTATT	AGCGCTGTTG	AAAGTCAGGT	TTGTTTGAGG	960
ATTACTCAAG	CGTTTGAGAG	TTTGAAATCT	CAATCTTTTG	AGAGCCAAAG	CGATCAACAA	1020
GACGCT						1026

(2) INFORMATION FOR SEQ ID NO:1414:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...759
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414

AACGCTCATG	CCTTTACCCA	TCCATTAGC	GCACCAGCTC	GCTTTCGCCT	AGCTCAAAAA	60
AGAAAAGACA	ACACCTTGCC	TTTTTTAAGG	CCTGATGGCA	AGTCTCAAGT	GAGCGTGCGT	120
TATGAAAACA	ACAAGCCTGT	AAGCGTTGAT	ACGATTGTCA	TTTCCACCCA	ACATTCCCCA	180
GAAGTTTCAC	AAAAGCATTT	AAAAGAAGCG	GTGATTGAAG	AGATCGTGTA	TAAGGTTTTA	240
CCCAAAGAAT	ATTTGCATGA	CAATATCAAG	TTTTTTATAA	ACCCTACAGG	AAAATTCGTC	300
ATCGGTGGGC	CTCAAGGCCA	TGCGGGTTTG	ACAGGTAGAA	AAATCATCTG	GGATACTTAT	360
GGAGGTTTTT	GCCCCATGG	AGGGGGAGCG	TTTACCGGGA	AAGACCCTTA	CAAGGTGGAT	420
ATGAGCGCGG	CTTATGCGGC	CCGCTATGTG	GCTAAAAATT	TGGTAGCGAG	CGGGGTTTGC	480
GATAAAGCGA	CCGTGCAGCT	TGCTTATGCG	ATTGGGGTGA	TAGAGCCTGT	GTCTATTTAT	540

SUBSTITUTE SHEET (RULE 26)

994

GTGAACACGC	ATAACACGAG	CAAGCATTCA	AGCGCGGAGT	TGGAAAAATG	CGTGAAATCG	600
GTTTTCAAAC	TCACGCCAAA	AGGCATCATT	GAAAGCTTGG	ATTGTGTAAG	ACCCATTTAT	660
TCGCTCACTT	CAGCTTATGG	GCATTTTGGG	CGCGAGTTAG	AAGAATTCAC	TTGGGAAAAG	720
ACTACAAGG	TTGAAGAGAT	TAAAGCGTTC	TTTAAGCGT			759

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415

TCAACAATTC	ACAAGGAGTT	TAAATTGAAA	CAAAGAACGC	TGTCTATTAT	TAAACCGGAT	60
GCACTTAAGA	AAAAAGTGGT	AGGCCAAAAC	ATTGATCGCT	TTGAGAGTAA	CGGCTTGGAA	120
GTGGTGGCCA	TGAAACGCTT	GCATTTGAGC	GTGAAAGACG	CTGAAAACCT	TTATGCGATC	180
CTCAGAGAGA	GACCCTTTTT	TAAAGATTGG	ATAGAGTTTA	TGGTGAGTGG	TCCGGTGGTG	240
GTTATGGTTT	TAGAAGGCAA	AGATGCGGTG	GCTAAAAACA	GAGAGCTTAT	GGGAGCGACT	300
GATCCCAAAC	TCGCCCAAAA	AGGTACTATC	AGAGCGGATT	TTGCTGAGAG	CATTGACGCT	360
AATGCGGTGC	ATGGGAGCGA	TAGCTTGGAA	AACGCGCACA	ATGAAATCGC	TTTCTTTTTT	420
GCCGCTAGAG	AGTTT					435

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416

GGCGGAGGTG	GAATTTATAT	TGAACATGGC	AGGGTTAAAA	TGGTAGCTTT	AAGCAACGCT	60
CTTTCAGGGG	TTTTTGTTTC	TGTGGCTGGC	TATAAATCC	CTTCTTTTAT	CCAAAAAAGC	120
ATCAACGCTC	TTTATGTTAA	GATCTTTAAA	ATTGATTGTA	GCGAGTTTGA	GCCTTTAGAA	180

995

AATTATAAGA	GTTTGAACGC	TCTTTTCATG	CGCTCTTTAA	AAAAAGAACG	CCCCTTTGAC	240
AAAGCCCCCTA	ATATTTGCAT	TGCGCCTTGC	GATGCTTTAA	TCACTGAATG	CGCTTTTTTA	300
GACAACGATA	GCGCTTTTACA	AATTAAAGGC	ATGCCCTATA	AAGCGCATGA	ATTAGTGGGC	360
GAAATCAACC	CCTTAAGCCC	TTCTTTTTC	TATGTGAATT	TTTACCTTTC	GCCCAAAGAT	420
TACCACCACT	ACCACGCCCC	TTGCGATTTA	GAAATTTTAG	AGGCTCGTTA	TTTTGCGGGG	480
AAATTACTAC	CAGTCAATAA	GCCCTCATT	CACAAAACA	AAAATCTGTT	TGTGGGCAAT	540
GAAAGGGTCG	CGCTTGTTGC	AAAAGACGAT	TCAAGGCAA			579

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417

AACCATAATA	AAGGGGCGGA	AATTCGCTA	TGGGGTTTAA	CCCGCTTGGT	GGATAGAGAC	60
ATTGATAAGG	ATAACCCAAG	GACGAAAAAC	CGCCCGAGCG	TGGATGGTAG	GATCAGCGTT	120
AAAGGCATGG	TCATTTTTAG	CGTTTCAAAC	GCTATTTTGT	TTGTGGGATG	GAGTAATTTT	180
ATCAACCCCT	TAGCTTTCAA	GCTTTCGTTA	CCTTTTTTAA	TCATTTTAGG	GGGGTATTTC	240
TATTTCAAGC	GCTTTTCCTC	TTTGCGCGAT	TTGTCTGTTG	GTTTGGCTTT	GGGTTTAGCC	300
CCCATTGCAG	GAAGCGTGGC	GGTTTTAGGG	GATATTCCTT	TATGGAATGT	CTTTTTGGCT	360
TTAGGGGTGA	TGTTGTGGGT	GGCTGGGTTT	GATTTGCTCT	ATCTTTTACA	GGATATGGAG	420
TTTGATAAAG	AAAGGGGCTT	GTTTTCCATT	CCTAGCCAAT	TAGGGGAAAA	ATGGTGCTTG	480
AATCTTTCAA	GGCTCTCGCA	CCTTGTTGCA	CTGATCTGCT	GGCTTTGTTT	TGTGAAATGC	540
TATCATGGGG	GGCTTTTTCG	GTATTTGGGC	TTAGGGGTTT	CAGCCTTGAT	CTTACTCTAT	600
GAGCAGATTT	TAGTGGCCAG	AGATTATAAA	AACATTCCCTA	AAGCCTTTT	TGTGAGTAAT	660
GGCTATTTGG	GGGTGGTGTT	TTTTATTTTT	ATCGTCCTTG	ATGTGGGGTT	CAAGCATGCA	720

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

996

(B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418

GTAATGGCTA	TTTGGGGGTG	GTGTTTTTTA	TTTTTATCGT	CCTTGATGTG	GGGTTCAGC	60
ATGCATGAGT	TGGTTTTAAG	ATCCCAAGCT	TTAGGGTTTG	AAACGCGCTT	AGTCCAGTGC	120
GATTTATCGT	TTTCTTATGA	AAGGTTTATT	TCTAAAACCA	AACGCTCTTT	AGCGGTGTTA	180
GAAGAAATTG	ATTGGTTAAA	TTCTGGCTTT	GATTTTTTAC	GCTTGAACGT	TGAAAATGAC	240
ACTCTGGAAT	TACTCAAAGC	GCTGTATTTT	AAATTAGAAA	AATTAGAGAG	CCTGCTTTTA	300
AAAGAAAATT	TACTTGAATT	GGAGCAAAAG	GATCGCATCA	TCGCTTTAGG	GCATGGGCTA	360
GTTTGCCCTA	AAAAACAAAG	CCTGATAGCG	CCTCAAACCT	ACTATGGGCG	TTGCGTGTTA	420
GAGGGGAAAA	TCCTAGCCTT	TTTTGGCGTG	GCAAGGGATA	AAGATTTTTT	AGAAATCACT	480
CGCATGCACG	CCTTAGACAT	TAAGCCTTAT	GATTCCTTCA	TTGTTGATAG	CGAAAGAAAA	540
GGCTTGAAAT	TA					552

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419

ACGGGAGCAA	TCATGTTATC	TTCTAATGAT	TTGTTTATGG	TCGTTTTAGG	GGCGATTTTA	60
TTGGTGTGG	TGTGCTTGGT	GGGGTATTTG	TATCTTAAAG	AAAAAGAGTT	TTACCATAAA	120
ATGAGGCGTT	TAGAAAAAAC	TTTAGATGAA	TCCTATCAAG	AAAATTATCT	CTATTCTAAG	180
CGTTTGAGAG	AATTAGAGGG	GCGTTTGGAA	GGCCTTTCTT	TAGAAAAAAG	CGCTAAAGAG	240
GACAGCTCAT	TAAAAACGAC	TCTTTCGCAC	CTTTATAACC	AGTTGCAAGA	AATCCAAAAA	300
TCCATGGATA	AAGAGCGCGA	TTACTTAGAA	GAAAAAATCA	TTACT		345

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

997

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420

GAGCCCATTA	AAAGCGACAA	AGAAGCCTTT	GATCTGGTCA	TGCAAAATCG	ATCGCATGAA	60
ATACAAGGCG	TATCACACAT	TAAGAATAAT	TATAAATTTT	TCACCAAAGA	GCTTGACAAT	120
TATATCAGCA	AAGGGTATCG	CATTGAAGAG	ATTATATGGCG	CGTTTTTGTG	GCTCAAAATC	180
GTAGCCATAG	GTTTAGAGTT	GGGCGAAGAC	GATCCGCAAG	TGGTGTGTTGA	GAGCATCAAC	240
GCTACAGGCG	TGCAATTAAA	AGGGCTGGAT	CTCATCCGCA	ACTATTTGAT	GATGGGGGAA	300
AATTCTGACA	ACCAGAATCG	TCTTTATAAT	ACTTATTGGG	TGCCTTTAGA	AAATTGGCTT	360
GGTGAAAAGG	ATTTGAATGA	TTTCATCAAA	ACCTATTTGA	GAATCTATTT	TGAGGATAGA	420
GTTAAAGAGG	GAGAGCGCGA	AGTGTATTAC	GCGCTAAAAG	CCCACCACAG	AGACAATTTT	480
CCTAACAAATA	TACAAGGTCT	TATGAGCGAT	ATGCGAGAAT	ATGGCAGAAT	CTTTCAAATC	540
TTTTTAGACA	GAGATCATT	TTTTTTACAT	CGTGAGAGCC	CGCAACAGTT	AGCGAATTTA	600
CGCTTGCGCG	TTAAAGATCT	CGTAAAATC	AAATTTGGCG	TGGCAAAGCC	CTTTGTTTTG	660
CGTTGCGCCA	GAGATTTTGA	AGAAGGCAAA	TGGATTATG	AAAACCTTCCA	TGAAATCTTG	720
CAAATCCTTA	TCAGTACTT	CGTGCGCCGA	AGCGTGTGCG	GGGATTCTAC	CCCTACGCTT	780
ACCAGAGTTC	TTTATTCTTT	ATACAGACAG	CTAGGGGAAG	ATGTTTCAGC	CGATGCATTG	840
AAGCGGTATT	TGGGCAAGAG	CGTTGGTCAA	ATGGCGTTCC	CTAATGACGA	TAAAATTAAA	900
GCGGCGTTTC	TTGTGCGTAA	CGCTTATGCA	GCAAATCAAG	TGTGCAAATT	CATCCTGCTT	960
GAGATTGAAA	AATTAGCAAC	GCTGAACCGC	CAAAGAAGA	GAATT		1005

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421

TTCTATGTCT	CGATCATTA	ATGCACGCCT	TTATTGGTCC	AAATCGTAAT	CGTGTTTTAT	60
GGTTTGCCCG	CCCTTGGGGT	CTATATGGAT	CCAATCCCGG	CAGGCATTAT	TGCGTTTCT	120
TTTAAATGTG	GGGCATACGC	TTCAGAGACT	TTGAGGGCGA	GCTTTCTTTC	TGTCCCTAAA	180
GATCAATGGG	ATTCAAGCTT	GAGTTTGGGC	TTGAATTACT	TGCAAACCTT	TTGGCATGTC	240
ATCTTTTTTC	AAGCGCTCAA	AGTCGCCACG	GCCAAGCCTA	AG		282

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

998

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422

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TCAATAAAAC ATTTAGGCAA AAAAGAGGTG AAAACCTTAG GATTGTCTTC GCTTGGTGGG      60
ACTTTAGAAAT TTTACGATTT TATCATCTTT GTATTTTITA CAAGTATCAT TGCCAAACAC      120
TTTTTCCCAA ACACGCTTAG CCTATCTGG TCTGAAATCA ACACTTATGG GATCTTTGCT      180
GCAGGTTATC TGGCGCGCCC GCTTGGTGGC ATAGTGATGG CCCACTTTGG GGATAAATTC      240
GGTCGTAAAA ACATGTTTCAT GCTCTCTATT TTATTAATGG TAATCCCAAC CTTTGCCTA      300
GCTTTGATGC CAACTTTTAA TGATTGGTG GGTTTTGGCG TGGATAGCAT GGGGCTTACC      360
CCTAAAAACG CTCATTATCT TGGTTACATA GCTCCTGTTT TTTTGGTGCT TGTTAGGATT      420
TGTCAGGCGC TCGCTGTGGG TGGTGAATTG CCTGGCGCTT GGGTTTTTGT CCATGAACAT      480
GCCCCACAAG GACAAAAAAA CACTTATATC GGTTTTTTAA CCGCTTCCGT AGTTTCTGGG      540
ATTTTGCTTG GGAGTTTGGT TTATATCGGG ATTTACATGG TTTTGGACAA GCCTGTGTGTT      600
GAAGATTGGG CTGGCGGGT TGCCTTTGGG CTGGAGGAA TTTTGGTAT CATTCTGTG      660
TATTTGAGGC GCTTTTAGA AGAAACTCCC GTTTTTCAGC AAATGAAGCA GGACGATGCC      720
TTAGTCAAAT TCCCGCTTAA AGAGGTGTTT AAAAATTCCT TCTTGGTAT ATCAATCTCC      780
ATGCTTATCA CTTGGGTTTT AACCCTTGT ATTTTGATT TTATCCTTTT TGTCCTGAAT      840
TTTACCCTTA CGCATCCCAA TTTTCATTT ACTCCGTTG AAAAAACCTA TTTTCAAATT      900
CTAGGACTTG TTGGTATTGT AAGTCTATT ATTTTCACCG GGTTTTTTGG TGATAAAATC      960
AAACCGCACA AAGTTTGCAT GGCTTTTAGC GCGGCCTTG GGTTTTTTGG CTTTATTTC      1020
TTTAAGGAAT TTTATTCTAA CGCGCCAAGT TTAGTCAATA CTATAATTTT ATACTTTTTTA      1080
GCTTGCTTTT GCGCGGGCAT TATGAATTTT TGCCCCATTT TCATGAGCGA TGTGTTTAGC      1140
GCTAGAAATCC GTTTAGCGG GATTTCCTTT GCTTATAACA TAGCCTATGC TATAACCGCT      1200
GGCTTTTACC CTCAACTTTC AAGCTGGTTA AACGCAAAAG CTATAGCAGT GCCTGAAAGT      1260
TTGCAAAGTT ATGGTTTAA CTTTATATC CTTATAGTTT CTTTAATTGC TTTTATTACA      1320
TCGCTTTTAA TGCGCCCAAT TTATCAGAAA TCTAATACCC AACACGAAAGT GTCGCCCACG      1380
GCA

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(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423

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AAATCGCTCA AAAAGAAGTG CCGGAGCTTT TTGCAAGAAT ATGAGGTTTA TTCTTTGGAT      60
TTGGCTTTTAA TGGTAGCTGG GGCAAAATAC AGAGGGGATT TTGAAAAGCG CCTGAAAAA      120
ACGCTCAAAG AGATCCAGCA AAACGGCCGT ATCATTTTAT TCATTGATGA AATCCACACC      180
CTTTTAGGTG CAGGGAGCAG TAACGCTGGG AGCTTGGATG CGGCGAATAT ATTAAACCG      240

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SUBSTITUTE SHEET (RULE 26)

999

GTTTTAACGG	ATGGGAGCTT	GAAATGTTTG	GGGGCGACCA	CTTTTGAAGA	ATACCGCAGC	300
GTGTTTGAAA	AAGACAAGGC	TTTCAACAGG	CGCTTTTCTA	TAGTGAATGT	TGAAGAGCCT	360
TCTAAGGAAG	CGTGTTACTT	GATTTTAAAG	AATATTGCCC	CCCTTTATGA	AGAACCAC	420
CAGGTGCGTT	ATAATGAAAG	CGTGTTTAAAG	GCATGCGTGG	ATTGACGAG	CTATTACATG	480
CATGATAAAT	TCTTGCCGGA	TAAGGCGATT	GAATTATTAG	ATGAGGTGGG	ATCAAGGAAA	540
AAGATCAACC	CTAAAAAAGG	CAAAAAATC	AGCGTTGATG	ACGTGCAAGA	AACGCTCGCT	600
CTCAAGCTTA	AAATCCCTAA	AATGCGTTTA	AATAGCGATA	AAAAAGCCCT	TTTAAGGAAT	660
TTGGAAAAAT	CGCTAAAAAA	TAAGATTTTT	GCCCCAACCG	AAGCGATCAA	CCTTGTCAGC	720
AATGCGATCA	AAATCCAGCA	TTGCGGGCTT	TCTGCAAAAA	ATAAGCCTGT	GGGGAGCTTT	780
TTATTCGTGG	GGCCTAGTGG	GGTAGGAAA	ACAGAATTGG	CTAAAGAATT	GGCCTTGAAT	840
TTGAATTGTC	ATTTTGAACG	CTTTGACATG	AGCGAATACA	AAGAAGCCCA	TAGCGTGCCA	900
AAGCTCATCG	AAGTCCCTAG	CGGTATGTG	GGGTTTGAGC	AAGGGGGGT	ATTGGTGAAT	960
GCGATTAAAA	AGCACCCGCA	TTGTTTGCTG	CTTTTAGATG	AGATAGAAAA	GGCCACCCT	1020
AATGTGTATG	ATTGTTGTT	GCAGGTGATG	GATAACGCCA	CTTTGAGCGA	TAATTTAGGC	1080
AACAAGGCGA	GTTTAAAGCA	TGTGATACTG	ATTATGACTT	CAAATGTGGG	GAGTAAGGAT	1140
AAGGACACGC	TAGGGTTTTT	TAGCACTAAA	AACGCCAAGT	ATGATAGAGC	CGTTAAAGAG	1200
CTTTTAACCC	CTGAATTGCG	ATCCAGAATT	GATGCGATCG	TGCCGTTTAA	CGCGCTCAGT	1260
TTGGAGGATT	TTGAACGCAT	TGTTTCTGTG	GAATTGGACG	GGTTAAAAGC	CCTAGCAATA	1320
GAGCAAGGCG	TGATCTTAAA	ATTCCATAAA	GAAGTTGTGA	AATGCATCGC	GCAAAAGAGC	1380
TACCAGAGGA	GTTTTGGTGC	GAGAGAAATT	AAAAAAATCA	TCAGAGGGA	AATCAACCCC	1440
CAATTAAGCG	ATATAGTGCT	TAAACAATCG	CTTAAAAAAC	CAACAAGATC	GTTGCGCATG	1500
AAGAGCACAT	TTCACAAAGT	G				1521

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424

GGAATAAAGT	TGATAAAATT	TGTGCGTAAT	GTGGTTTAT	TCATTTTAAC	AGCGATCTTT	60
TTAGCGTTCA	TGCTTTTAGT	GAGTTATTGC	ATGCCCCATT	ATAGCGTGGC	TGTCATTAGC	120
GGGGTGGAAG	TCAAAAGAAT	GAATGAAAAT	GAAAACACGC	CCAATAATAA	GGAAGTAAAA	180
ACCCTTGCTA	GAGATGTCTA	TTTTGTGCAA	ACTTACGACC	CTAAGGATCA	AAAAAGCGTG	240
ACCGTCTATC	GTAACGAAGA	CACGCGCTTT	GGCTTCCCTT	TTTATTTTAA	GTTTAATTCTG	300
GCTGATATTT	CAGCTCTCGC	TCAAAGTTTA	GTCAATCAGC	AAGTGGAAAGT	GCAATACTAT	360
GGCTGGCGGA	TCAATTTGTT	TAACATGTTT	CCTAATGTGA	TTTTTTTAAA	ACCCTTAAAA	420
GAGAGCGATG	AGATGTCAAA	ACCCGTTTTT	AGCTGGATTT	TATACGCCCT	GCTACTAGTG	480
GGCTTTTTTA	TCAGTGCACG	TTCTGTTTGC	ACTTTATTTA	AGGGCAAAGC	TCAT	534

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

1000

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425

CGCGGCTTTT	TATTGTATAA	TCTTAAAAAT	TTTATTAAAG	GAAAAAGTTC	AATGTCTAAT	60
CAAGAATACA	CCTTCCAAAC	TGAAATCAAC	CAGCTTTTGG	ATTGATGAT	CCACTCTTTG	120
TATTCTAATA	AAGAGATTTT	TTTAAGGGAG	TTGATTTCTA	ACGCGAGCGA	CGCTTTGGAT	180
AAGCTGAATT	ATTTGATGCT	AACCGATGAG	AAATTAAAG	GGCTGAATAC	CACGCCTAGC	240
ATCCATTTGA	GTTTTGATAG	CCAAAAA	ACCTTAACGA	TAAAGACAA	TGGTATAGGC	300
ATGGATAAAA	GCGATCTCAT	CGAGCATTTA	GGCAGCATCG	CTAAATCAGG	CACGAAGAGT	360
TTTTTAAGCG	CTTTGAGTGG	GGATAAGAAA	AAAGATAGCG	CCTTAATTGG	CCAATTTGGC	420
GTGGGCTTTT	ATTCGGCGTT	CATGGTAGCG	AGTAAGATTG	TCGTTCAAAC	CAAAAAAGTT	480
ACCAGTCAATC	AAGCTTATGC	ATGGGTGAGC	GATGGTAAGG	GCAAGTTTGA	AATCAGCGAA	540
TGCGTCAAAG	AGGAGCAAGG	CACAGAAATC	ACCCTCTTTT	TAAAAGAAGA	AGATTCTCAT	600
TTTGCGAGCC	GTTGGGAGAT	TGATAGCGTT	GTTAAAAAGT	ATTCTGAGCA	TATCCCTTTC	660
CCTATTTTTT	TAACTTACAC	CGATACGAAA	TTTGAGGGCG	AAGGGGATAA	TAAAAAGAA	720
GTTAAGAAG	AAAAATGCGA	TCAGATCAAT	CAAGCGAGCG	CTTTATGGAA	AATGAATAAG	780
AGCGAATTGA	AAGAAAAGGA	TTACAAAGAC	TTTTACCAAT	CGTTTGCACA	TGATAACAGC	840
GAGCCTTTGA	GCTATATCCA	TAATAAAGTG	GAAGGCTCTT	TAGAATACAC	GACGCTTTTT	900
TATATCCCTA	GCAAAGCGCC	CTTTGATTGG	TTTAGGGTGG	ATTATAAAAG	CGGGGTCAAA	960
CTTTATGTTA	AACGGGTGTT	TATCACTGAT	GATGACAAAG	AATTGTTGCC	GTCTTATTTG	1020
AGGTTTGTGA	AAGGCGTGAT	TGACAGCGAA	GATTTGCCCT	TGAACGTGAG	TCGTGAAATC	1080
TTACAGCAGA	ATAAGATTTT	AGCCAATATC	CGTTCGGCTT	CAGTGAAAAA	GATTTTAAGC	1140
GAGATTGAAA	GGCTGAGCAA	GGATAACAA	AATTACCATA	AATCTATGA	GCCTTTTGGG	1200
AAAGTGTTAA	AAGAAGGCTT	GTATGGGGAT	TTTGAAAAA	AAGAAAAACT	TTTAGAATTG	1260
TTGAGATTCT	ATTCTAAAGA	CAAAGGAGAA	TGGATTCTT	TAAAAGAATA	CAAAGAAAAT	1320
TTAAAAGAAA	ATCAAAAAAG	CATTTACTAC	CTTTTAGGCG	AAAATTTAGA	CTTATTAAAA	1380
GCGTCCCCCC	TTTTAGAAAA	ATACGCTCAA	AAAGGCTATG	ATGTTTGTG	ATTGAGCGAT	1440
GAAATTGATG	CGTTTGTGAT	GCCAGGCGTG	AATGAATACG	ATAAAACGCC	CTTTAGAGAC	1500
GCTAGCCATA	GTGAGAGTTT	GAAAGAGCTT	GGTTTGGCAG	AAATCCATGA	TGAGGTAAAA	1560
GATCAGTTTA	AAGATTTAAT	CAAAGCGTTT	GAAGAAAATC	TTAAAGATGA	GATTAAGGGC	1620
GTAGAGCTTT	CTGGTCATCT	CACCTCAGCG	GTGGCTTTAA	TAGGCGATGA	ACCAAATGCG	1680
ATGATGGCTA	ATTGGATGCG	TCAAATGGGG	CAAAGCGTGC	CTGAAAGCAA	GAAAACTTTA	1740
GAATTAAACC	CTAACCATGC	GATTTTGCAA	AACTCTTAA	AATGCGAAGA	TAAAGAGCAG	1800
TTGAGCGCTT	TTATCTGGTT	GCTTTATGAT	GGGGCGAAGC	TTTTAGAAAA	AGGGGCTTTA	1860
AAAGACGCTA	AAAGTTTAA	CGAACGCTA	AATAGCGTGC	TATTGAAGGC	GTTG	1914

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

1001

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426

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AAGCAATTTG GTAGGCGAGT TTTTACCCAA ATTCTTAAAA TGGTGCAATT TCAAAACACG      60
CTTATAAAAT TCCATGCCCT ATCCTTTTAAA AACGCAAAT TAATTATATA TGCAAAATTA      120
AACAAAACAT GCTATAAAGA AAATTCAAAT ACTATCATT TAAGGATTAA AATGCTCACC      180
CAAGAAGATG TCTTAAACGC GTTAAAAACG ATCATCTACC CTAATTTTGA AAAGGATATT      240
GTCAGCTTTG GTTTTGTTAA AAACATCACC TTGCATGACA ACCAATTAGG GCTTTTAAATA      300
GAAATCCCCT CAAGCTCTGA GGAAACGAGT GCGATTTTAA GGGAAAATAT CTCCAAAGCG      360
ATGCAAGAAA AAGGCGTGAA AGCTTTGAAT TTGGATATTA AAACCCCGCC TAAACCGCAA      420
GCTCCAAAGC CCACCACTAA AAATCTGGCT AAAAACATCA AGCATGTGGT CATGATAAGC      480
TCAGGCAAGG GCGGTGTGGG TAAAAGCACC ACCAGCGTGA ATTTAAGCAT CGCTTTAGCG      540
AATTTAAACC AAAAAGTGGG GCTACTAGAC GCTGATGTGT ATGGCCCTAA TATCCCTAGA      600
ATGATGGGCT TGCAAAACGC TGATGTGATC ATGGATCCTA GCGGTAAAAA ACTCATTCCT      660
TTAAAAGCTT TTGGCGTTTC TGTGATGAGC ATGGGGCTTT TGTATGATGA GGGGCAGAGT      720
CTCATTTTGA GAGGACCCAT GCTCATGCGA GCCATTGAGC AGATGCTAAG CGATATTATT      780
TGGGGGGATT TAGACGTGCT GGTGGTGGAT ATGCCCCCAG GAACAGGCGA TGCGCAGCTC      840
ACGTTAGCCC AAGCCGTGCC ACTCAGCGCA GGAATCACCG TTACTACGCC TCAAATCGTG      900
AGTTTAGATG ACGCTAAACG GAGTTTGGAC ATGTTTAAGA AACTACACAT TCCTATTGCG      960
GGCATTGTAG AAAATATGGG GAGTTTGTG TGGGAGCATT GCAAGAAAGA GAGCGAGATT      1020
TTTGGCTCAA ATTCCATGAG TGGATTATTA GAGGCTTATA ACACGCAGAT TTTAGCCAAG      1080
CTCCCTTTAG AGCCTAAAGT GCGTCTAGGG GGGGATAAGG GTGAACCGAT TGTGATTCT      1140
CATCCCACTA CCGTGAGTGC TAAAATTTT GAAAAAATGG CAAAGGATTT GAGTGCCTTT      1200
TTAGACAAGG TGGAAAGGGA AAAACTAGCC GATAATAAGG ACATCCAGCC CACACAAACG      1260
CATGCTTATT CGCAT

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(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427

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CTAGGGTTTT TGGCTTTGCA TGGGTTTTTT CTCAGCGCTT TTGAGTATCA AGTGAGCGCT      60
AGAGTGGGAT CGTTTTTCGG TATCGCTTTC AACCAATCGA TCATCAATT CAAAAAAGGG      120
ATTTACCCTA CAGGGAGTTA TGTAACCACT ACCGGGGCTT TACAAGTTGA TTCTAGTTTG      180
CTCCCTAAAG GGATTGAAAA CCACAAATG GGTTTTGGGG TGGGGGGCGA AATAGGAGCG      240
TTAGCTTATG ATTCCACGAA ATTTTGTGAT GATGAAGCCA ACCCTAAGGC AGGGTTTCAG      300
CCAGCGAAGT GGTATTACAT GGGGCGATGG GAGGGCTATT TGATGCAACA CAGCCAAAAT      360
TGGACCAGAG AGCAAAAGGC TCAAAACGCC AGGCCTTATG TGTTATACAA TTTGTATTTA      420
GATTATCAAT ATAAGGACAT TTTTGGGATT AAAGTAGGGC GTTACCCTTC TAAGGCTTTG      480
TTTTTGAGCG GGTTTAATCA AGGGTTTGAG ATTTTTTACC GGTGAAAAAA GTTTAAGATA      540
GTGTGGTTTA GCACCTTTGG AAGGGCTTTA GCCAATGAGC AATACATTAG GGATTTTTCAC      600

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SUBSTITUTE SHEET (RULE 26)

1002

GCTCCTGTCA	ATTACAAGCA	AAAAATCAAC	TACGGCATGC	ACAATTTCAA	CCTCGTTTAC	660
GAAAATAAAT	ACATTAGGAT	CGCGCCTTTT	ATTTGGTTTT	ACCCTAAGAA	TTTTAACGCT	720
CCTGGATTTG	AAATCACCCA	TGACACAAAA	TCCTATTGGA	AATCTCTTTG	GCGCATCCAA	780
ACGACTTTTT	ACGCATGGTT	TCCTCTCTAT	AGCGACTATT	TGTCTAAAGA	TTATTATAGG	840
GCCGCTTTAG	TGGGTAAAAA	AAGCGCGGCT	TTGTTTGTGT	TTCAAAGAGT	GAATTTCCGC	900
TCCTATCGTT	TTGGCTGGAG	CGTGATAAAG	AATTTTGGGA	ACGCGAGCGT	TCAGTTAGGT	960
TGGAATGGCT	CACCCATTGA	TCCTTTTTAC	GACACGAAAG	ATGATACCCC	TTATGAAGAC	1020
GCTTATTCCA	ATTTTTACAA	CGCTAATTCC	ATAACGATTA	ACGCTTTTAT	AGGGAAGAGC	1080
ATTAAGAATC	TTTTGGTGCA	ATTGTATGGG	AAATTAACCT	ATTCCCCAAG	GGCTGATGCG	1140
CAAAGCTTAG	GGGTTACTTT	TAAATATAAC	CTTAAAAAAC	ATATCTATTT	CATGCTAATG	1200
GTTAATGGCT	ATCAAATCAC	GATGCATAAG	GGTTATAAGG	TAGGGTTTTT	TACAAGCGGT	1260
TACAACCTTG	ATTTGCTCA	AACCATTCAA	AATAGAAGCT	ATTTGATGAG	CTCTATGAGT	1320
TATCGTTTT						1329

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428

TACCCTACAA	ATACTATTAT	TGAAAGGATT	TTGATGTTTA	AAAAAATGTG	TTGAGCCTG	60
CTAATGATAA	GCGGTGTTTG	TGTGGGGGCA	AAGGATTTGG	ATTTCAAGCT	GGATTATCGC	120
GCGACTGGGG	GGAAATTCAT	GGGGAAAAATG	ACGGACTCTA	GTCCTTTAAG	TATCACTTCT	180
ATGAACGATG	AACCGGTGGT	GATTAAAAAC	CTTATTGTCA	ATAGGGGAAA	TTCAGTCGAA	240
GCGACTAAAA	AAGTAGAACC	CAAATTTGTC	GATAAGTTTA	AAAAAGAAAA	ACTCTTTGAT	300
CATGAATTAA	AATACTCGCA	ACAGATATTT	TACCGCCTGG	ATTGCAAGCC	TAACCAATTG	360
TTAGAAGTTA	AAATCATCAC	GGACAAGGGC	GAATATTACC	ATAAATTTTC	CAAA	414

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429

AGGATTGGCA	TGGACGCTTT	AGAAATCACC	CAAAAACCTCA	TCAGTTACCC	TACCATTACG	60
CCCAAAGAAT	GCGGTATTTT	TGAATACATT	AAATCGCTTT	TTCTTGCTTT	TAAAACCCTA	120
GAATGTGAAA	AAAATGGCGT	GAAAAACCTT	TTTTTATACC	GCATTTTAA	CCCCCTCAA	180
AAGCATGCAG	AAAAAGAACA	TGCAAAAGAA	AAGCATGTAA	AAGAAAATGT	TAAGCCCTTG	240
CATTTTGTCT	TGTCAGGGCA	TATTGATGTC	GTGCCTCCTG	GGAACAATTG	GCAAAGTGAT	300
CCCTTTAAAC	CCATCATTA	AGAGGGGTTT	TTATACGGTC	GTGGGGCGCA	AGACATGAAG	360
GGGGGCGTTG	GGGCGTTTTT	GAGTGCGAGT	TTAAATTTTA	ACCCTAAAC	CCCTTTTTTG	420
CTTTCTATTT	TACTCACGAG	CGATGAAGAA	GGGCCAGGGA	TTTTTGGCAC	TAGGCTTATG	480
CTAGAAAAAC	TCAAAGAAAA	GGATTGCTG	CCTCATATGG	CGATTGTGGC	TGAACCCACT	540
TGCGAAAAAG	TCTTAGGCGA	TAGCATCAAA	ATTGGCCGAA	GAGGCTCTAT	TAATGGCAAA	600
CTCATTTTAA	AAGGCGTTCA	AGGGCATGTG	GCTTACCCGC	AAAAATGCCA	AAACCCTATT	660
GATACGCTCG	CTTCAGTTTT	GCCTCTCATT	TCAGGAGTTC	ATTTAGACAA	TGGCGATGAG	720
TGTTTTGACC	CTTCAAAATT	AGTCATCACC	AACTTGCATG	CAGGGTTAGG	GGCTAATAAT	780
GTTACACCAG	GGAGCGTAGA	AATGCGCTTT	AATGCGCGCC	ATTCTTTAAA	AACCACCCAA	840
GAGAGTTTGA	AAGAATATTT	GGAAAAGGTT	TTGAAAGATT	TGCCCTTATAC	TTTAGAATTA	900
GAATCAAGCA	GTTTCGCCCTT	CATCACGGCT	TCCCATTCAA	AGCTTACTAG	CGTTTTACAA	960
GAAAAATATTT	TAAAAACATG	CCACACCACC	CCCCTTTTAA	ACACCAAAGG	CGGCACGAGC	1020
GATGCGCGAT	TTTTTAGCGC	TCATGGTATA	GAAGTGGTGG	AGTTTGGCGC	CATTAATGAC	1080
AGGATCCATG	CCGTTGATGA	AAGGGTGAGC	TTGAAGGAAT	TAGAGCTTTT	GGAAAAAGTG	1140
TTTTTGGGGG	TTTAGAGGG	CTTGAGCGAG	AAA			1173

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...2784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430

ACAAGCCTTG	ATCACAAAAT	CACAGATTTT	TCTTGCCTGG	ATTTGAGGAT	CCAATCTAAA	60
GAAGTCAGTC	ATAATTTAAA	GGAATTATCA	AAAACGCTAA	TCAGCTATCC	TTTTGAAAAA	120
CATGTAGAAG	CTTTAGGGGA	ACAATGCAGT	AACCTCGTTT	CTATTCCCAT	TAACAATGAC	180
GACTATTCAA	ATATTTCAC	TTTTGTGAGT	GATTTTATAA	ATCTTATAGC	TTCTTACAAT	240
TTATTAGAAT	CATTTTLAGA	TTTTTATAAA	GATAAATTAA	AATTGAGCGA	GCTTGTAAT	300
GAATATGCCA	ACGTAACCAA	TAATCTGCTT	TTCAAAAAAT	TAATCAAACA	TTTAAGCGGC	360
AACAATCAAT	TGGTTAAAAA	TTTTTATCAG	TGTATAAGAG	AAATTATAAA	ATACAACGCC	420
CCTAATAAAG	AATACAAACC	CAATCAATTT	TTTATAATAG	GGAAAGGCAA	ACAAAAACAA	480
TTAGCAAAAA	TTTTATTCTCA	TTTAAAAGAA	CTTAGTGCAA	GTGAAATTAA	ACCACAAGAT	540
ATGGAAGACA	TCTTAAAAAA	GCTAGAGGAA	TTAGATAAAA	TTTTTAAAAAC	TACCGACTTT	600
ACAAAATTCA	CACCAAAAAC	TGAAATTAAG	GATATTATTA	AAGAAATAGA	CGAAAAATAC	660
CCTATCAATG	AAAATTTTAA	ACGGCAATTT	AATGAGTTTG	AATCAAAATAT	TGAAAAACAT	720
GATGAAATAA	AAAAGGATTT	TGAGCGAAAC	AAAGAGTCGC	TGATCCGAGA	AATTGAAAAAT	780
CACGTCAAAA	ATGAATGCAA	TAGCGAAGAA	GAGCCGGAGT	ATAAGATTAA	TGATCTGCTC	840
AAAAATATCC	AACAAATATG	CAAAAATTAT	ATAGAAAGTC	ATGCCGTTAA	TGATGTGTCT	900

SUBSTITUTE SHEET (RULE 26)

1004

AAAGATATTA	AATCCATGAT	GTGTCAGTTT	TATTTGAAAC	AGATAGATTT	ATTAGTCAAT	960
TCAGAAATTG	TGCGATACAG	ATACAGCAAT	CTTTTGAAC	CAATACAAAG	ATCTTTATGG	1020
GAGAGTATAA	AAATTTTGA	TAATGAAAGT	GGCATTTATT	TGTTCCCTAA	AAATATTGGT	1080
GAAATCAAGG	ATAAATTGA	AGCAAACAAG	GAAAAATTCA	AACAAAGCAA	AAATGTTTCT	1140
GAGTTCGCAG	AATATTGCCG	AGAGTGTAA	CCCTATACAG	CGTTTAACTT	TCATCTAAAT	1200
ATAAATAATG	GTCTATCTCA	TCAATTTGAA	AAATTCGTGC	CAATCATGAA	AGAATACAAA	1260
GAGCCAAAAA	TCACAGATAA	TGACCTTGAA	GCCATATCAA	CCAAAGAGAC	TGGTCTTGCT	1320
AGCCAATTAT	CTGGGCACTG	GTTTTTTCAG	CTTTCGTTAT	TTAATAAAAC	AACTTTTAAT	1380
CCTAATAAAA	TTTGGATTCC	TTTAGAGTTC	AATAAAAGAT	CAAAAATAAA	GTTTGATAAA	1440
GATTTAGAAA	TCTATTTTGA	TAGTCATGAA	TCGTTCAATA	TCTCTAAAAA	ATACTTGCAA	1500
GAAATAGATC	AAGAATCACT	AAAAAAGATC	AAACAATCAA	AAGATTTTTT	TTCAATTCAA	1560
AAAAATAGAGA	GTAAGCATGA	TAATAACGAT	ATACTGCAAC	TTGAATTTTT	TGAGAATGAT	1620
ACAAGTTTTT	TTTTTGCTAA	AGGAAGTTTT	GCAGAAATTT	TAGAATACAA	CATGCAATTA	1680
AAAAATAGATT	CTTTAATTAC	AAAAGAATTT	AATAAGCTTT	TAGCGATCGT	TCAAGATAGT	1740
CCCCAAGATA	GTTACCAATT	AAAATTTCGT	GTCCGACATA	ACAATAAGCT	TCCTAGAGAG	1800
AAATATACGG	AACATGAAAT	AAAATTGAA	GTTTATGATT	GCAGAAAAATC	CCACGATCAC	1860
AATGAGCCAA	TCATCTTAAG	CCAGCAAAGC	ACCGGCTTCC	AATGGGCGTT	TAATTTTCATG	1920
TTTGCGTTTT	TTTATAATGT	GGGATCACAT	TTTAGTTTTA	ACCATAATAT	TATCTATGTC	1980
ATGGACGAGC	CAGCCACTCA	TTTGAGCGTG	CCAGCCAGAA	AGGAGTTTAG	GAAATTTTTA	2040
AAAGAATACG	CTCATAAAAA	TCATGTTACT	TTTGTTTTAG	CCACCCATGA	CCCCTTTTTA	2100
GTGGATACGG	ATCATTTAGA	TGAAATAAGG	ATTGTGGA	AGGAAACAGA	AGGCTCTGTA	2160
ATTAAGAATC	ACTTTAATA	TCCCTAAAT	AATGCAAGCA	AAGACTCCGA	CGCTTTGGAC	2220
AAAATCAAAAC	GCTCTTTAGG	AGTGGGCCAG	CATGTTTTTC	ATAACCCCA	AAAACACCGA	2280
ATCATTTTTG	TAGAAGGCAT	CACGGATTAT	TGTTATTTGA	GCGCTTTTAA	ATGTATTG	2340
CGTTACAAAG	AATACAAGGA	CAACCCATT	CCTTTCACCT	TCTTACCCAT	TTCAGGGCTT	2400
AAAAACGATT	CAAACGATAT	GAAAGAAACC	ATTGAAAAAC	TTTGCGAGTT	AGACAATCAC	2460
CCTATTGTTT	TGACAGACGA	TGACAGAAAA	TGCGTTTTTA	ACCAACAAGC	AACGAGCGAA	2520
CGATTTAAAA	GAGCTAATGA	AGAAATGCAT	GATCCCATCA	CCATCCTACA	ACTCTCAGAC	2580
TGCGATAGGC	ATTTCAAACA	AATTGAAGAT	TGTTTCAGCG	CAAACGATAG	AAACAAATAC	2640
GCTAAAAATA	AGCAAATGGA	ATTGAGCATG	GCTTTTAAAA	CAAGGCTTTT	GTATGGCGGA	2700
GAAGATGCCA	TAGAAAAACA	AACAAAAAGA	AATTTTTTAA	AATTATTCAA	ATGGATTGCA	2760
TGGGCTACAA	ACTTGATCAA	AAAC				2784

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431

CAAGCATTTG	GTATCAATAT	GTGTTCTAAA	AAAATAAGAA	ATCTCATTTT	ATGCTTTGGT	60
TTTATTTTAA	GCTTGTGCGC	TGAAGAAAAT	ATCACCAAAG	AAAACATGAC	TGAAACGAAC	120
ACGACTGAAG	AAAACACCCC	TAAAGACGCT	CCCATTCTTT	TGGAAGAAAA	ACGCGCCCAA	180
ACTCTAGAGC	TTAAAGAAGA	AAATGAAGTG	GCAAAAAAGA	TTGATGAAAA	AAGCCTGCTT	240
GAAGAAATCC	ATAAGAAAAA	ACGCCAGCTT	TACATGCTCA	AAGGGGAATT	GCATGAAAAG	300
AATGAATCCA	TCATTATTCCA	ACAAATGGCT	AAAAATAAGA	GCGGCTTTT	TATAGGCGTG	360
ATCCTTGGCG	ATATAGGGAT	TAACGCTAAT	CCTTATGAGA	AGTTTGAAC	TTTAAGCAAT	420
ATTCAAGCTT	CTCCCTTGCT	GTATGTTTTA	AGGAGCGGGT	ATCAAAAGTA	TTTCGCTAAC	480

SUBSTITUTE SHEET (RULE 26)

1005

GGGATTAGCG CCTTACGCTT TTATGGGGAA TATTTAGGGG GGGCGATGAA AGGGTTTAAA	540
AGCGATTCTT TAGCTTCTTA TCAAACCGCA AGCTTGAATA TTGATCTGTT GATGGATAAG	600
CCTATTGACA AAGAAAAAAG GTTTGCGTTA GGGATATTTG GAGGCGTTGG AGTGGGGTGG	660
AATGGGATGT ATCAAAATTT AAAAGAGATT AGAGGGTATT CACAGCCTAA CGCCTTTGGG	720
TTGGTGTTAA ATTTAGGGGT GAGCATGACG CTCAACCTCA AACACCGCTT TGAATTAGCC	780
CTAAAAATGC CTCCCTTAA AGAACTTCG CAAACCTTTT TATATTATTT TAAAAGCACT	840
AATATTTATT ATATTAGTTA CAACTATTTA TTG	873

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432

AGATTTTTTA GAAAGCATAG GGTATAAGC ATGAAAGAAA TCGTTACAAT AGAGAATGTG	60
TCTTTTAACT ACCACAATCG CGCTATTTTT AAGGATTTTA ATTTAAGCAT TCAAGAAGGG	120
GATTTTTTAT GCGTTTTAGG GGAGAGCGGG AGCGGTAAAA GCACGCTTTT AGGCTTGATT	180
TTAGGGCTTT TAAACCCAG TCTGGGGAGC GTTAAATCT TTAATGAGAC CCTTTCAAAC	240
AACGCTTTTT TACGCCAAAA AATAGGCTAT ATCGCTCAGG GCAATTCCTT ATTCCCTCAT	300
TTAAACGCCT TACAAAACAT GACTTTTTGC CTTAATTTAC AAGGCATAAA CAAACAAGCC	360
GCTCAAAAAG AAGCCAAAGC CTTAGCGTTA AAAATGGGGT TAGACGAGAG CCTTATGGAT	420
AAATTCCTTA ATGAATTGAG TGGGGGGCAA GCCCAAAGAG TGGGCATTAT TAGGGGGATT	480
ATCCACAGGC CAGAACTCAT TTTATTAGAT GAGCCTTTTA GCGCTTTAGA TAGTTTGAAT	540
CGTAAGAATT TACAGGATCT CATCAAAGAA ATACACCAAA ATTCTTGCGC TACTTTCATT	600
ATGGTAACGC ATGATGAAAA CGAGGCGCAA AAGTTAGCCA CAAAAACCCT AGAAATCAAA	660
GCCCTTAAAC AAGAGCAG	678

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

1006

(B) LOCATION 1...1782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433

ATGGCTGATT	TATTGTCCAG	TTTGAAAAAC	CTTCTAGTA	GTAGTGGGGT	GTATCAATAT	60
TTTGATAAAA	ACCGCCAATT	ACTCTACATC	GGTAAGGCGA	AAAATTTAAA	AAAGCGCATC	120
AAAAGCTATT	TTTCTGTCCG	TAATAATGAA	ATCACGCCCA	ATCCTCGCAC	AAGCTTACGC	180
GTCCAAATGA	TGGTCAAACA	GATCGCTTTT	TTAGAAACCA	TTTGTAGTGA	AAACGAGCAA	240
GACGCTTTGA	TTTTGGAAAA	TTCTTTGATC	AAGCAGCTCA	AGCCTAAATA	CAACATTCTT	300
TTAAGAGACG	ATAAACTTA	CCCTTATATT	TACATGGATT	TTTCTATTGA	TTTCCCTATC	360
CCTTTAATCA	CACGAAAAAT	CTTAAACAG	CCTGGCGTTA	AATATTTTGG	CCCTTTTACG	420
AGCGGGGCTA	AGGATATTTT	GGACAGCTTG	TATGAATTGC	TCCCTTTGGT	TCAAAAGAAA	480
AATTGCATCA	AGGATAAAAA	GGCATGCATG	TTTTATCAAA	TAGAGCGITG	TAAAGCCCCA	540
TGCGAGGATA	AAATCACTAA	AGAAGAATAT	TTAAAAATCG	CTAAAGAAATG	TTTAGAAATG	600
ATTGAAAATA	AAGACAGGCT	CATCAAAGAG	CTTGAATTGA	AAATGGAGCG	CCTTTCTAGT	660
AACTTGCGTT	TTGAAGAAGC	CTTAATTAT	AGGGATAGGA	TTGCAAAAAT	CCAAAAATC	720
GCCCTTTTCA	CTTGCAATGA	TTTAGCCAAA	CTCTACGATT	TGGATATTTT	TGCTTTTAT	780
GGTGGAACA	ACAAGGCGGT	GTTAGTAAA	ATGTTTCATG	GTGGGGGTAA	AATCATTCT	840
TCAGCGTTTG	AAAAAATCCA	CTCTCTCAAC	GGGTTTGACA	CTGATGAAGC	GATGAAACAA	900
GCCATTATCA	ATCATTACCA	ATCGCATTTG	CCTTTGATGC	CTGAACAAAT	CTTATTGAGC	960
GCTTGTCTTA	ATGAAACGCT	TAAAGAATTG	CAAGAGTTTA	TCTCTCACC	ATATTCTAAA	1020
AAAAATCGCTC	TTAGCATTC	TAAAAAGGGT	GATAAGCTCG	CTTTAATAGA	AATCGCTATG	1080
AAAAACGCTC	AAGAGATTTT	TAGCCAAAGAA	AAAACCTCTA	ATGAAGATCG	GATCTTAGAA	1140
GAAGCGCGAT	CGCTCTTCAA	TTTAGAGTGC	GTGCCTTATA	GGGTAGAAAT	CTTTGACACA	1200
AGCCACCATT	CAAACAGCCA	ATGCGTGGGG	GGATGGTTCG	TGTATGAAAA	CAATGCATTT	1260
CAAAAAGACT	CTTATCGGCG	CTACCATCTA	AAAGGCTCTA	ACGAATATGA	TCAAATGAGC	1320
GAATTGCTCA	CCAGAAGGGC	TTTAGACTTT	GCTAAAGAGC	CACCGCCTAA	TTTGTGGGTG	1380
ATAGATGGAG	GGAGGGCGCA	ATTAAACATC	GCTTTAGAAA	TTTTAAAAAG	CAGCGGGAGT	1440
TTTGTAGAAG	TGATCGCTAT	TTCTAAAGAA	AAAAGGGATT	CTAAGGCTTA	TCGTTCTAAA	1500
GGGGGTGCTA	AAGACATTAT	CCATACGATT	AGTCATACTT	TTAAATTGCT	CCCTAGCGAC	1560
AAACGCTTGC	AGTGGGTGCA	AAAATTGCGC	GATGAAAGCC	ACCGGTATGC	GATAAACTTC	1620
CATAGATCCA	CTAAACTTAA	AAACATGAAA	CAATCGCTC	TTTTAAAAAG	AAAGGGCATA	1680
GGAGAAGCCA	GCGTGAAAAA	ATTGTTGGAT	TATTTTGGGA	GTTTTGAAGC	GATAGAAAAA	1740
GCGAGCGATC	AGGAAAAAAA	CGCGGTTTTA	AAAAACGAA	AA		1782

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434

AGGAAAAACA	TGAAAAAAG	ATTGAATATA	GGGCTTGTGG	GTTTAGGGTG	CGTGGGGAGC	60
ACGGTCGCTA	AAATCTTACA	AGAAAAATCAA	GAAATCATTA	AAGACAGAGC	CGGCGTGGA	120
ATTAAAAATTA	AAAAAGCGGT	GGTGCAGAGC	GTGAAAAAAC	ACAAGGGCTA	TGCTTTTGAA	180
ATCAGTGATG	ATTTAGAAAG	CGTGATAGAA	GATAAAGGGA	TTGATATTGT	CGTGGAGCTT	240
ATGGGTGGGG	TGGAAGCGCC	TTATCTTTTA	GCTAAAAAAA	CTTTAGCCAA	ACAAAAAGCC	300
TTCTTACAG	CCAATAAAGC	CATGTTAGCG	TACCACCGCT	ATGAATTAGA	ACAAATCGCT	360

SUBSTITUTE SHEET (RULE 26)

1007

AAAAACACCC	CCATAGGCTT	TGAAGCGAGC	GTGTGTGGGG	GTATCCCAT	TATCAAGGCT	420
TTAAAAGACG	GCTTGAGCGC	TAATCACATC	CTTTCTTTTA	AAGGGATTTT	AAACGGCACG	480
AGCAATTACA	TTTTAAGCCA	GATGTTTAAA	AATCAAGCGA	GCTTTAAGGA	CGCTTTGAAA	540
GACGCGCAGC	ATTTAGGCTA	TGCGGAATTG	AACCCTGAAT	TTGACATTAA	GGGCATTGAT	600
GCGGCGCACA	AATTATTGAT	TTTAGCGTCT	TTAGCGTATG	GCATTGATGC	GAAATTAGAA	660
GAAATCTTGA	TTGAAGGCAT	TGAAAAGATA	GAGCCAGATG	ACATGGAATT	TGCAAAAGAG	720
TTTGGTTATA	GCATCAAAC	TTTAGGCATC	GCTAAAAAAC	ACCAGGATTG	CATTGAATTA	780
AGGGTGCATC	CAAGCATGAT	TAAAAATGAA	TGCATGCTCT	CTAAAGTGGA	TGGGGTGATG	840
AACGCTATCA	GCGTCATAGG	GGATAAGGTG	GGCGAGACTT	TGTATTATGG	GGCTGGGGCT	900
GGAGGAGAGC	CTACCGCAAG	CGCGGTCATT	AGCGATATTA	TAGAAATCGC	AAGGAAAAAA	960
AGCTCTCTAA	TGCTGGGCTT	TGAAACCCCT	CAAAAACTCC	CCCTAAAACC	CAAAGAAGAA	1020
ATCCAATGCG	CTTACTATGC	GCGCTTGTTA	GTGAGCGATG	AAAAAGGGGT	TTTTTCTCAA	1080
ATCAGCGCCA	TTTtagccca	AAATGATATT	TCGCTCAACA	ATGTCTTGCA	AAAAGAAATC	1140
CCGCAATCCA	ACAAGGCTAA	AATCTTATTT	TCCACGCACA	CCACCAACGA	AAAATCTATG	1200
CTGAACGCCC	TTAAAGAGCT	TGAAAATTTA	CAAAGCGTGT	TGGATACCCC	TAAAATGATC	1260
CGTTTGAAAA	AT					1272

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435

AGTCGCTTTA	AAAGAGCAAT	TGAACAAGCT	TTTAGGCTAG	TGGCCATGAT	AGATTGCGCG	60
ATTATTGGAG	GTGGTCCGTC	AGGTTTGAGT	GCGGGGCTTT	ATGCCACTAG	AGGCGGTGTT	120
AAAAACGCCG	TTTTATTGTA	AAAAGGAATG	CCTGGGGGGC	AAATCACTGG	CAGTAGTGAG	180
ATTGAAAAAT	ATCCGGGCGT	TAAGGAAGTG	GTGAGCGGAT	TGGATTTCAT	GCAACCATGG	240
CAGGAGCAAT	GCTTTCGCTT	TGGTTTAAAG	CATGAGATGA	CCGCCATTCA	AAGGGTTTCT	300
AAAAAAGGTT	CTCATTTTGT	TATTTGGGCA	GAAGATGGCA	AGACTTTTGA	AGCTAAGAGC	360
GTGATCATCG	CTACCGGTGG	TAGCCCTAAA	CGCACAGGTA	TCAAGGGCGA	GTCAGAATAT	420
TGGGGTAAAG	GCGTTAGCAC	TTGTGCAACA	TGCGATGGCT	TCTTTTACAA	AAATAAGGAA	480
GTAGCGGTGC	TTGGTGGAGG	CGATACCGCC	GTAGAAGAGG	CGATTTATCT	AGCCAATATC	540
TGCAAAAAAG	TCTATCTCAT	CCACAGAAGA	GATGGTTTTA	GGTGTGCGCC	TATCACTTTA	600
GAGCATGCTA	AAAACAATAG	TAAGATTGAG	TTTTTAACCC	CTTATGTGGT	GGAAGAAATC	660
AAGGGCGATG	CTTCTGGCGT	GTCTTCTTTA	AGCATTAATA	ACACAGCCAC	TAACGAAAAA	720
AGAGAATTAG	TCGTGCCGGG	GCTTTTTATT	TTTGTGGGTT	ATGATGTGAA	TAACGCCGTG	780
TTGAAGCAAG	AAGATAACTC	CATGCTATGC	GAATGCGATG	AATACGGCTC	TATTGTCTGT	840
GATTTTTCCT	TGAAGACGAA	TGTTCAAGGC	TTGTTTGC	CGGAGATAT	TCGCATTTTT	900
GCCCCAAGC	AAGTGGTTTG	TGCGGCAAGC	GATGGTGCTA	CGGCAGCCTT	AAGCGTGATT	960
TCTTATTAG	AACACCAT					978

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

1008

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436

AAATTATGGG	AGTTTAGCTT	GCGTGTTCCTT	ATCATTTCTT	TAAATCAAAA	AGTGTGCGAT	60
AAATTGAGTT	TGGTTTTTAG	AGACACCACA	ACTTTACTCA	ATAATATCAA	CGCCACCCAC	120
CACCAAGCGC	AAATTTTGA	TGCGATTTAT	TCCAAGACTT	TTGAAGGCGG	GTTGCACCCC	180
CTAGTTAAAA	AGCATTTACA	CCCTTATTTC	ATCACGCAAA	ATATCAAAGA	CATGGGGATT	240
GCAACCCAGTC	TCATCAGTGA	GGTTTCTAAG	TTTTATTACG	CTTTAAAATA	CCATGCGAAA	300
TTTATGAGCT	TGGGGGAGCT	TGGGTGCTAT	GCGAGCCATT	ATTTCGTTGTG	GCAAAAATGC	360
ATAGAGCTCA	ATGAAGCGAT	CTGTATTTTA	GAAGACGATA	TAACCTTGAA	AGAGGATTTT	420
AAAGAGGGCT	TGGATTTTTC	AGAAAAACAC	ATCCAAGAGT	TAGGCTATGC	GCGTTTGATG	480
CATTATTGT	ATGATGCCAG	CGTGAAAAGT	GAGCCTTTAA	ACCATGAAAA	CCAAGAGATA	540
CAAGAGCGTG	TGGGGATCAT	TAAAGCTTAT	AGCCATGGGG	TGGGGACGCA	AGGCTATGTG	600
ATCAGCCCCA	AGATTGCCAA	AGTTTTTTTG	AAACACAGCC	GAAAATGGGT	TGTTCTCTGTG	660
GATACGATAA	TGGACGCTAC	TTTTATCCAT	GGCGTGAAAA	ATCTGGTGTT	ACAACCTTTT	720
GTGATCGCTG	ATGATGAGCA	AATCTCTACG	ATAGCGCGAA	AAGAAGAACC	CTATAGCCCT	780
AAAATCGCTC	TAATGAGAGA	ACTCCATTTT	AAATTTTGA	AATGTTGGCA	GTTTGTA	837

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437

GGGGATTTTA	TAATTTCTAA	CATCAGCATA	CACCCAAAAA	CCATGTTTAA	AAACGCTTTA	60
AATATACAAG	ATTTTTCATT	TAAAAATCAT	ACTAGTACAG	CCATTATTGG	CACAAATGGT	120
GCTGGAAAAT	CAACGCTTAT	CAACACTATT	CTAGGCATTA	GATCAGACTA	TAATTTTAAA	180
GCACAAAACA	ATAATATTCC	ATACCAAGAC	AATGTTATAC	CACAACGCAA	GCAATTGGGA	240
GTGTCTCTA	ACCTATTCAA	CTACCCACCT	GGATTAAACG	CAAACGACCT	TTTTAAATTC	300
TATCAATTTT	TTCAAAAAA	CTGCACTCTA	GATTTGTTTG	AAAAAAATCT	TTTAAATAAA	360
ACCTACGAAC	ACCTAAGCGA	CGGACAAAAA	CAGCGCTTAA	AAATTGACTT	AGCTCTTAGC	420
CATCACCCAC	AATTAGTTAT	TATGGATGAA	CCAGAAACCA	GTTTAGAGCA	AAACGCTCTT	480

SUBSTITUTE SHEET (RULE 26)

1009

ATAAGACTAT CAAATCTCAT AAGCTTGCGC AACACCCAAC AACTTACAAG TATCATCGCC	540
ACTCATGATC CTATTGTCTT AGATAGTTGC GAATGGGTAT TGCTCCTTAA GAATGGCAAC	600
ATTGCTCAAT ACAAACCTTT AAATTCTATA TTAAATCTG TAGCTAAAAC TTTTAACTTT	660
AAAGAAAAAC CAACCACAAA AGACTTATTA GCGTTACTAA AGGATATT	708

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438

ATTATTCCTC ATCTCGCTCC CATTATGCAC TATCAATTAA CAAGTTTCAA TATAATACAA	60
GATCTTTTTA TAACTTGTC TGTGTTAAGG ATCAAAATGC GCGTGTTTGT TTGCTTTTTA	120
GGGGTTTTTG TATCTAACGG CTTGGGCTCGT TTTGGCTATG TGGTTTTAAT CCCCCTACTC	180
ATTTTATCAG GGAGTTTAAC CCCACACCAA AGCTTCCAAC TGGGTATTGC GGTGCTAATG	240
GGCTATGTTT TTGGGAGCTT TTTAATCCAA TTTTAAAGCC CGTTAATGTC ATTAGAAAGC	300
ATCGCTAAAA TCAGTTTTAA ATTAATCACT TTGAGTTT	339

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439

AGTATGGGCG GATTACAAAG CATATGGCAT TGGGTCATTG TTTTATTAGT GATTGTGTTG	60
TTATTTGGGG CTAAAAAGAT CCCAGAATTG GCTAAAGGTT TAGGCAGTGG GATTAAGAAT	120
TTCAAAAAAG CCGTGAAAGA CGATGAAGAA GAGGCTAAAA ACGAGCTAAA AACCCTAGAC	180
GCTCAAGCAA CACAAACCAA AGTGCATGAA ACTAGCGAAA TTAAAGCAA ACAAGAAAGT	240

SUBSTITUTE SHEET (RULE 26)

1010

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440

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AGAAAAACCA ACCACAAAAG ACTTATTAGC GTTACTAAAG GATATTTAAT GGGTGCAATT      60
TTATCTATTT TAAAACTTGA AATCAAATCT TATCTCACCA ATACAAGCGC GCTATTTTGG      120
ACTTTTATTT ATCCTATTTT AATGCTCCTA TTACTAATTT TTGTTTTTTC AAAAAATACC      180
ACTGAAATTT TTTACTTTAA TAACATTATA GGTCTAATGG GACTTCTTAT TATTTCTAGC      240
GCGATCTTTG GTCTCACACA AGCTATAACA AGCTCTAGAT CGCATAATAT ATTCTTATTC      300
TACATGCTAT CACCAGCAAC TTCAAACAA ATAACCTCTAG CATTAAATCGC TTCAAGACTA      360
ATCGTTGTAA TCCTATATGC TTTTATCTTT ATTGTTCTCT CTTTTTATGC GCTCAATATC      420
ATCACTATTC TTAATTTTAA AGCGCTTATT TTGGGGTTTA TTAGCATTTT TTCAAGCGCA      480
TTGTTTTGTT TTTGCTTGGC AATTTTTTGT GCTAGAATTT TTCAAAACGA ACAAAGCATC      540
TTAGGATTTT GTAATATCAT CAATCTCTAT GCGCTAATGT CTTGTAATGT TTTTGTTCTT      600
TTAGAATACC TACCTAATAT TGGTCAATTA TTTATCAAAA CATCTATTTT TTACTACCTT      660
AATCAACTTC TAATCAAAGC TTTTCAAGGG ATTGATACTA TACTGGTTTT AGCAACTTCA      720
ACATTTTTC TATTGGTGG CATTATTTTA TTTTACTAA GCGCTAATCG CATGTTACTA      780
ACACCAAAG AACGCATGCG T                                     801

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(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441

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AGAAAAACAAG AAATGAAAAA ACTTCTTTTA CTCTTAGAGC ATAAGATCGT AAAAAATGGC      60
TTAATTATTG TGATTGTGTT AGTGGGTTTT TTTCTTTTTT ATGAACAAGA AATCAAAGAA      120

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SUBSTITUTE SHEET (RULE 26)

1011

AAAGCTGTTA	ATGTTTCTCA	AGGTAAATTC	CCCACTTCAT	CTTATTTGTT	TCAAGCTTAC	180
GAAGGCATTA	AGAATAAAAT	AGATACTATC	AATCAAGTGA	AGCCAAACGA	TGAAACTAAA	240
AGCGTTAATG	AGAATATAGA	AAAAACACAA	AAAGATTTAG	ATGATTTTAA	TGCGCTAGTG	300
CAAAAGTTAC	CAAATTTGCC	TAAGGACTTT	AATAAAACAC	TTATTAAACC	ACAAAGTCCA	360
TTTTTCAACT	ACAATACCGC	TAACGAAGAT	GAAAAAAACC	GCCTGGTGAT	TTTAGCGTCT	420
CGTATTAGCA	GCCAAAAAGA	AACGCAACCT	CCCATTCTTA	TAAAAAATAG	CGTTTCTCAC	480
ATAAAATCCA	AAGAAAAACG	AGAACTTGAA	AAAGAATGGG	CAAAACCTAG	TGTTTCTTTT	540
GGTCTTTTTT	CCTTGCCTTC	CAGTCTCTCT	TCTTTTCTTT	CTTTTGAAGT	TTCTTTTTTA	600
TCAAGGGGAA	TAGGATTGGA	TTGTGAGAAG	CTCAAATCCT	TTTTAAAAGC	TTTTTCAAGT	660
TCGCTATTTT	CCTTATTATC	TTCATTGTTT	TGCCATCCAC	TTTCTCTTTT	TTGCTCTCTA	720
ATAGGATTAA	TCTTTTGTTT	TTCTAAGTTT	TCTAGAGAGC	TAGTGAATGC	GTCTAACAAAT	780
TCGCTTGAGT	TTTCATCATT	GTCAAGGCTA	GGATCA			816

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442

AAAATCTTCA	AAAAGGCTTT	AAGGCATAAA	ATGGAAAAAG	TTTGCGTGAG	CGCATGGGGG	60
TTGCCTAAGA	TTTTAGAAGA	AAGATTAAAA	GAAAAATATG	GCGATGATTG	GGAAAAACAT	120
GTTAAGGCTA	AAGCAATAAA	CGAAGAAGAG	CTTGAAGAAC	AAGTCAAAGC	TAAAGCCAAA	180
GAGCAACAAA	AGACACAAAG	AGAAAAACA	CTCAATGGAT	TTTTAAAAAA	AGTTGGTTTA	240
AAAAAGCGTG	ATATGTTACA	AAGCACTATG	TTATTTGATG	AAGTCAAAGA	AGCTGATGTG	300
CTTTTTCAAG	CAGAGCGTAA	AATTGGCGAT	TGGATTTTTA	GCAGTCCGGT	GTTCTTTTTT	360
GCTCTAGCCC	TTATAGAAGC	CATTATTATT	GTATGCTTAT	TGCCGTTAAA	AGAAAAAGTG	420
CCTTATTTAG	TAACCTTTTC	AAACGCTACA	CAAATTTTGT	CCATAGTCCA	AAGAGCAGAC	480
AAGAGCATCC	GTGCTAATCA	AGCGCTTG TG	AGACAATTGG	TAGCGTCTTA	TGTTAATAAT	540
AGAGAAAATA	TTTCAAGTAT	AAAAGAGCAA	AACGAAATAG	CCCACGAAAC	CATTAGGTTG	600
CAAAGCGCAT	TTGAAGTG TG	GGATTTTTTT	GAAAAACTGG	TTTCTTATGA	GCATAGCATT	660
TACACTAATA	TAAATCTAAC	ACGAAAAATT	AGCATTATCA	ATATCGCTTT	AATCAGTAAA	720
ACCCAAGCCA	ATATTGAAAT	ATCCGCACAA	CTTTTTTCATA	AAGAAAAAGTT	AGAAAGCGAA	780
AAGCGTTATA	GAATAATTAT	GACCTTTGAA	TTTGAACCTA	TTGAAATTGA	TACAAAATCT	840
GTTCCCGCTA	ACCCCTACAGG	CTTTATTGTT	ACAGGTTATG	ATGTAAGTGA	AATTGCGATT	900
TTAAAGATT	TAGATGAGAA	AAATAAAGTC	AAAGATGATG	GTGTGAAATC	TAGGATTATC	960
CATGTCGAGA	AAAAAGACCC	TCATATGAGC	CAGTATAAAG	ATGTTAAGGA	GCAA	1014

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

1012

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443

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GTTGTGTTAA TAAGGTTAGT CCTAAACATG CTAACATGTC AAATTAGCTA TATAAGGATA      60
AGTTATCTTG TCTCTGTTAG CGATTTTGTG ATTTGCAAGG AAAGATTATG GGATGAAATT      120
AAAACGCTGT TAGTGGATTG TTTCCCGCAG GCAAAGCATT TTGGGATAAT CTTAATCAAG      180
GCTATTGTTG TCTTTTGTAT AGGTTTTTAT TTTTCGTTTT TCTTACGGAA CAAAACCATG      240
AAACTCTTAT CCAAAAAGGA TGAGATTTTG GCGAATTTTG TCGCGCAGGT TACTTTTATC      300
TTAATCCTTA TCATTACTAC AATCATCGCG CTCAGCACGC TAGGCGTCCA AACCACCTCT      360
ATTATCACTG TTTTAGGAAC GGTGGGGATT GCGGTGGCGT TGGCTTTAAA AGATTATCTT      420
TCAAGCATTG CTGGAGGGAT AATCCTTATT ATTTTACACC CTTTCAAAA AGGAGACATC      480
ATTGAAATCT CTGGCCTAGA GGGCAAAGTA GAAGCGCTTA ATTTTITTA TACTTCTTTA      540
CGCTTGCATG ACGGGCGCTT GCGGTTTTG CCTAATAGAA GTGTCGCTAA TTCTAATATT      600
ATCAATAGCA ATAACACTGC GTGTCGGCGC ATTGAATGGG TCTGTGGGGT AGGGTATGGG      660
AGCGATATTG AACTGGTGCA TAAGACTATA AAAGATGTTA TTGACGGGAT GGAAAAAATT      720
GATAAAAACA TGCCCCACTT CATTGGAATC ACGGATTTTG GACAAAGTTC GCTGAAC TTC      780
ACCATTAGGG TTTGGGGCAA GATTGAAGAC GGGATCTTTA ATGTGAGGAG CGAACTCATT      840
GAACGCATCA AAAACGCCCT GGACGCTAAT CGTATTGAAA TCCCTTTCAA CAAGCTAGAT      900
ATTTCTATCA ACAAACAAGA CTCTTCTAAG      930

```

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444

```

AGCAAAAGAA CACAACAAAC CTTTTTCTA TTCATGATG AAACATAAGA CTACATTATG      60
CATCCTATAA TGTTTGCTTA TATCGCTAAC GCGCTCGCTC AAGCTAGAAA GATCAACGGA      120
ACACTTTGCA TGGCGTTTCA AAAAATATCT CAAGTCAAAG AATTAGGCAT TGATAAAGCA      180
AAGAGTTTGA TAGGCAACCT TTCTCAAGTG ATTATCTACC CCACAAAAGA TACTGATGAA      240
TTAATAGAAT GTGGCGTCCC ATTAAGCGAT AGTGAAATCA ATTTCTTACA CAACACGGAC      300
ATGAGAGCCA GACAAGTGCT AGTAAAAAAT ATCGTTACAA ACGCTTCAGC TTTTATTGAA      360
ATTGATTTAA AAAAGATTG CAAGAATAC TTTATATTCT TGATAGCAAT GCTGGTAATA      420
GAAAAATCCT CAATGATCTT AAAAAAGCAA ACCAAGAAAC TTATAAGGAA GAGTATT      477

```

SUBSTITUTE SHEET (RULE 26)

1013

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445

```

CTCCTTAAAA ATATTGATGA GAAAAAGCTT TCCGTAAGTA AGGTAAATGA AAAAAGGCAC      60
ATGGATTTTA AAAAATGCCC TAATTTTGAA AAAAAATGTG CGTTTCTTTG TTTCTCAAAT      120
TTGGTTTTAC TTATTGAAAT CCACTCTAAA GGACTACACA TGCAAAAAAA GAAACCCAAG      180
AACCCGCAAC CGAATTTATT TAGCATCTTA GATAAGGGCG ATGTTGCAAC AAACAATCCT      240
GTTGAAGAGT CAGACAAGGC CAATAAAATA CAAGAGCCAC TCCCTTATGT CGTGAAAACG      300
CAATCAATA AAGCAAGCAT GATTTCTAGA GATCCTATTG AATGGGCAAA GTATTTAAGC      360
TTTGAAAAAC GAGTCTATAA GGATAATAGT AAAGAAGATG TCAATTTCTT TGCCAATGGT      420
GAGATAAAAG AAAGTTCTCG TGTTTATGAA GCGAATAAAG AAGGGTTTGA AAGGCGCATC      480
ACTAAAAGAT ACGATCTGAT TGATAGAAAT ATTGATAGAA ATAGAGAATT TTTTATAAAA      540
GAAATTGAAA TTCTAACCCA CACAAACAGC TTAAGAAGAT TGAAAGAGCA AGGGTTAGAA      600
ATCCAATTGA CCCACCATAA TGAAACGCAT AAGAAAGCCT TAGAAAATGG CAATGAAATC      660
GTTAAAGAA ACGACCATCT TAAAGATATT TACCAAGAAG TAGAAAGAAC AAAAGATGGT      720
GGATTGGTAA GAGAAATAAT CCCAGTATT TCTAGCGCTG AGTATTTCAC CCTT          774

```

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446

```

Asp Ala Arg Ser Phe Phe Leu Arg Leu Val Ala Met Ala Leu Cys Leu
1           5           10          15
Ile Leu Ile Asn Ser Arg Gly Val Ala Met Gly Tyr Ala Ser Lys Leu
20          25          30
Ala Leu Lys Ile Cys Leu Val Gly Leu Cys Leu Phe Ser Thr Leu Gly
35          40          45
Asp Glu His Leu Glu Gln Lys Gly Asn Tyr Ile Tyr Lys Gly Glu Glu

```

SUBSTITUTE SHEET (RULE 26)

1014

```

      50              55              60
Ala Tyr Asn Asn Lys Glu Tyr Glu Arg Ala Ala Ser Phe Tyr Lys Ser
65              70              75              80
Ala Ile Lys Asn Gly Glu Ser Leu Ala Tyr Ile Leu Leu Gly Ile Met
      85              90              95
Tyr Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val Glu
      100              105              110
Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn Asn
      115              120              125
Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu Lys
      130              135              140
Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr Asn
145              150              155              160
Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val Pro
      165              170              175
Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His Lys
      180              185              190
Gly Asn Val Glu Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser Gly
      195              200              205
Asn Asp Gln Leu Gly Ile Glu Pro Asp Lys Asp Lys Ala Val Val Tyr
210              215              220
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Glu Gly Leu
225              230              235              240
Ser Glu Pro Tyr Arg Tyr Gly Leu Gly Val Glu Lys Asp Lys Lys Lys
      245              250              255
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
260              265              270
Cys Lys

```

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447

```

Thr Met Lys Asn Thr Ser Ser Ser Thr Thr Leu Thr Met Asn Asp Thr
1              5              10              15
Ile Ala Ala Ile Ala Thr Pro Leu Gly Lys Gly Ala Ile Ser Ile Ile
      20              25              30
Lys Ile Ser Gly His Asn Ala Leu Asn Ile Leu Lys Gln Leu Thr Gln
      35              40              45
Lys Gln Asp Phe Thr Pro Arg Tyr Ala Tyr Val Cys Asp Ile Phe Ser
50              55              60
Asp Gly Val Leu Leu Asp Lys Ala Leu Val Ile Tyr Phe Lys Ala Pro
65              70              75              80
Tyr Ser Phe Thr Gly Glu Asp Val Cys Glu Ile Gln Cys His Gly Ser
      85              90              95
Pro Leu Leu Ala Gln Asn Ile Leu Gln Ala Cys Leu Asn Leu Gly Ala
100              105              110

```

SUBSTITUTE SHEET (RULE 26)

1015

Arg Leu Ala Lys Ala Gly Glu Phe Ser Lys Lys Ala Phe Leu Asn His
 115 120 125
 Lys Met Asp Leu Ser Glu Ile Glu Ala Ser Val Gln Leu Ile Leu Cys
 130 135 140
 Glu Asp Glu Ser Val
 145

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448

Asn Leu Ile Tyr Arg Ser Ser Gln Arg Ser Ala Ala Ala Cys Val Val
 1 5 10 15
 Arg Leu Asn Lys Glu Pro Met Ile Glu Tyr Leu Lys Ser Asn Ile Lys
 20 25 30
 Leu Ile Asp Glu Met Ile Ala Ser Gly Tyr Glu Asp Lys Glu Thr Leu
 35 40 45
 Lys Lys Arg Arg Asp Ala Met Gln Ala Trp Val Asp Lys Pro Val Leu
 50 55 60
 Leu Glu Pro Asp Ser Asn Ala Gln Tyr Ala Ala Val Ile Glu Ile Asp
 65 70 75 80
 Val Ala Glu Ile Thr Glu Pro Ile Leu Ala Cys Pro Asn Asp Pro Asp
 85 90 95
 Asp Val Ala Thr Leu Ser Glu Val Leu Ala Asp Thr Thr Gly Lys Arg
 100 105 110
 Pro His Ala Ile Asp Glu Val Phe Ile Gly Ser Cys Met Thr Asn Ile
 115 120 125
 Gly His Phe Arg Ala Phe Gly Glu Ile Val Lys Asn Ala Pro Pro Ser
 130 135 140
 Gln Ala Arg Leu Trp Val Val Pro Pro Ser Lys Met Asp Glu Gln Glu
 145 150 155 160
 Leu Ile Asn Glu Gly Tyr Tyr Ala Ile Phe Gly Ala Ala Gly Ala Arg
 165 170 175
 Thr Glu Val Pro Gly Cys Ser Leu Cys Met Gly Asn Gln Ala Arg Val
 180 185 190
 Arg Asp Asn Ala Val Val Phe Ser Thr Ser Thr Arg Asn Phe Asp Asn
 195 200 205
 Arg Met Gly Arg Gly Ala Lys Val Tyr Leu Gly Ser Ala Glu Leu Gly
 210 215 220
 Ala Ala Cys Ala Leu Leu Gly Arg Ile Pro Thr Lys Glu Glu Tyr Met
 225 230 235 240
 Asn Leu Val Ser Glu Lys Leu Glu Ser Gln Lys Asp Lys Ile Tyr Arg
 245 250 255
 Tyr Met Asn Phe Asn Leu Met Glu Asn Phe Arg Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:1449:

SUBSTITUTE SHEET (RULE 26)

1016

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449

```

Lys Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Leu Leu
1           5           10          15
Phe Phe Leu Ile Val Cys Met Ile Asn Leu His Ala Lys Ser Tyr Leu
20          25          30
Phe Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro
35          40          45
Cys Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe
50          55          60
Ser Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys
65          70          75          80
Thr Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala
85          90          95
Ser Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala
100         105         110
Ile Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met
115         120         125
Asn Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile
130         135         140
Gln Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Glu Thr
145         150         155         160
Tyr Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Ile Ile Ala Leu Leu
165         170         175
Thr Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Asn Thr
180         185         190
Pro Thr Tyr Val Pro Thr Val Asn Lys Thr Gln Leu Glu Asn His Thr
195         200         205
Glu Leu Ser Leu Ser Glu Arg Leu Tyr Phe Gly Gly Ile Asp Tyr Lys
210         215         220
Glu Gln Leu Gly Met Leu Ala Thr Phe Ile Ser Pro Asn Ser Pro Val
225         230         235         240
Ile Glu Tyr Asp Asp Asp Gly Leu Ile Gly Glu Arg Leu Arg Gln Ile
245         250         255
Thr Glu Ser Leu Asn Val Glu Val Lys His Gln Glu Asn Ile Ser Tyr
260         265         270
Lys Gln Ala Thr Ser Phe Ser Lys Asn Phe Arg Lys His Asp Ala Phe
275         280         285
Phe Lys Asn Ser Thr Leu Ile Leu Asn Thr Pro Thr Thr Lys Ser Gly
290         295         300
Leu Ile Leu Ser Gln Ile Gly Leu Leu Glu Tyr Lys Pro Leu Lys Ile
305         310         315         320
Leu Ser Thr Gln Ile Asn Phe Asn Pro Ser Leu Leu Leu Leu Thr Gln
325         330         335
Pro Lys Asp Arg Lys Asn Leu Phe Ile Val Asn Ala Leu Gln Asn Ser
340         345         350
Asp Glu Thr Leu Ile Glu Tyr Ala Ser Leu Leu Glu Ser Asp Leu Arg
355         360         365

```

SUBSTITUTE SHEET (RULE 26)

1017

```

His Asp Trp Val Asn Tyr Ser Ser Ala Ile Gly Leu Glu Met Phe Leu
 370                               375                               380
Asn Thr Leu Asp Pro His Phe Lys Lys Ser Phe Gln Glu Ser Leu Glu
385                               390                               395                               400
Asp Asn Gln Val Arg Tyr His Asn Gln Ile Tyr Gln Ala Leu Gly Tyr
                               405                               410                               415
Ser Phe Glu Pro Ile Lys Asn Glu Ser Glu Thr Lys Lys Glu
                               420                               425                               430

```

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450

```

Tyr Leu Asp Asn Tyr Leu Asn Thr Phe Ile Phe Asn Gly Phe Leu Arg
1                               5                               10                               15
Lys Ile Asp Tyr Tyr Ala Ser Gly Lys Leu Lys Arg Ile Gly Ala Val
                               20                               25                               30
Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr Asn
35                               40                               45
Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala Glu
50                               55                               60
Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys Glu
65                               70                               75                               80
Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu Gln
85                               90                               95
Val Asp Ser Asn Leu Leu Pro Lys Asn Ile Glu Lys His Ser Leu Lys
100                              105                              110
Ile Gly Val Gly Gly Ile Leu Gly Ala Leu Ala Tyr Asp Ser Thr Lys
115                              120                              125
Thr Leu Ile Asp Gln Ala Thr His Gln Ile Tyr Gly Ser Glu Leu Phe
130                              135                              140
Tyr Leu Ile Gly Arg Trp Gly Phe Leu Gly Asn Ala Pro Trp Lys
145                              150                              155                              160
Asp Ser Leu Ile Glu Ser Asp Ala His Thr Arg Asn Tyr Val Leu Tyr
165                              170                              175
Asn Ser Tyr Leu Phe Tyr Ser Tyr Gly Asp Lys Phe His Leu Lys Leu
180                              185                              190
Gly Arg Tyr Leu Ser Asn Met Asp Phe Met Ser Ser Tyr Thr Gln Gly
195                              200                              205
Phe Glu Leu Asp Tyr Lys Ile Asn Ser Lys Ile Ala Leu Lys Trp Phe
210                              215                              220
Ser Ser Phe Gly Arg Ala Leu Ala Phe Gly Gln Trp Ile Arg Asp Trp
225                              230                              235                              240
Tyr Ala Pro Ile Val Thr Glu Asp Gly Arg Lys Glu Val Tyr Asp Gly
245                              250                              255
Ile His Ala Ala Gln Leu Tyr Phe Ser Ser Lys His Val Gln Val Met
260                              265                              270
Pro Phe Ala Tyr Phe Ser Pro Lys Ile Tyr Gly Ala Pro Gly Val Lys

```

SUBSTITUTE SHEET (RULE 26)

1018

```

      275              280              285
Ile His Ile Asp Ser Asn Pro Lys Phe Lys Gly Leu Gly Leu Arg Ala
 290              295              300
Gln Thr Thr Ile Asn Val Ile Phe Pro Val Tyr Ala Lys Asp Leu Tyr
305              310              315
Asp Val Tyr Trp Arg Asn Ser Lys Ile Gly Glu Trp Gly Ala Ser Leu
      325              330              335
Leu Ile His Gln Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Phe Gly
      340              345              350
Tyr Tyr Gln Asn Phe Gly Asn Ala Asn Ala Arg Ile Gly Trp Tyr Gly
      355              360              365
Asn Pro Ile Pro Phe Asn Tyr Arg Asn Asn Ser Val Tyr Gly Gly Val
      370              375              380
Phe Ser Asn Ala Ile Thr Ala Asp Ala Val Ser Gly Tyr Val Phe Gly
385              390              395
Gly Gly Val Tyr Arg Gly Phe Leu Trp Gly Ile Leu Gly Arg Tyr Thr
      405              410              415
Tyr Ala Thr Arg Ala Ser Glu Arg Ser Ile Asn Leu Asn Leu Gly Tyr
      420              425              430
Lys Trp Gly Ser Phe Ala Arg Val Asp Val Asn Leu Glu Tyr Tyr Val
      435              440              445
Val Ser Met His Asn Gly Tyr Arg Leu Asp Tyr Leu Thr Gly Pro Phe
      450              455              460
Asn Lys Ala Phe Lys Ala Asp Ala Gln Asp Arg Ser Asn Leu Met Val
465              470              475
Ser Met Lys Phe Phe Phe
      485

```

(2) INFORMATION FOR SEQ ID NO:1451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451

```

Val Tyr Ala Gly Leu Ala Ile Ala Ile Gly Met Leu Ile Asp Ser Ser
1              5              10              15
Val Val Val Val Glu Asn Ala Phe Glu Lys Leu Ser Ala Asn Thr Lys
      20              25              30
Thr Thr Lys Leu His Ala Ile Tyr Arg Ser Cys Lys Glu Ile Ala Val
      35              40              45
Ser Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe Val Pro Ile
      50              55              60
Leu Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro Leu Ala Gln
      65              70              75              80
Ser Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser Ile Thr Ile
      85              90              95
Ile Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro His Ser Glu
      100             105             110
Thr Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro Leu Leu Glu
      115             120             125

```

SUBSTITUTE SHEET (RULE 26)

1019

```

Phe Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala Phe Val Phe
130      135      140
Leu Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys Asn Phe Met
145      150      155      160
Pro Ala Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu Thr Thr Pro
      165      170      175
Ser Ile Ser Leu Asp Gln Ser Lys Asp Leu Met Leu Asn Ile Glu Ser
      180      185      190
Ala Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val Ala Arg Thr
      195      200      205
Gly Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn Gln Thr Asp
      210      215      220
Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val Lys Thr Lys
225      230      235      240
Asp Glu Leu Val Arg Lys Asn His Gly Phe Phe Lys Arg Leu
      245      250

```

(2) INFORMATION FOR SEQ ID NO:1452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452

```

Trp Leu Phe Leu Thr Cys Tyr Gly Ser Val Ile Lys Lys Gly Tyr Ile
1      5      10      15
Arg Gly Asp Leu Met Arg Ile Val Arg Asn Leu Phe Leu Val Ser Phe
      20      25      30
Val Ala Tyr Ser Ser Ala Phe Ala Ala Asp Leu Glu Thr Gly Thr Lys
      35      40      45
Asn Asp Lys Lys Ser Gly Lys Lys Phe Tyr Lys Leu His Lys Asn His
      50      55      60
Gly Ser Glu Thr Glu Thr Lys Asn Asp Lys Lys Leu Tyr Asp Phe Thr
      65      70      75      80
Lys Asn Ser Gly Leu Glu Gly Val Asp Leu Glu Lys Ser Pro Asn Leu
      85      90      95
Lys Ser His Lys Lys Ser Asp Lys Lys Phe Tyr Lys Gln Leu Ala Lys
      100      105      110
Asn Asn Ile Ala Glu Gly Val Ser Met Pro Ile Val Asn Phe Asn Lys
      115      120      125
Ala Leu Ser Phe Gly Pro Tyr Phe Glu Arg Thr Lys Ser Lys Lys Thr
      130      135      140
Gln Tyr Met Asp Gly Gly Leu Met Met His Ile Arg Phe
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
 (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

1020

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453

```

Pro Lys Ile Ala Pro Leu Ala Met Ala Leu Asn Pro Lys Thr Phe Gln
1      5      10      15
Pro Leu Trp Ile Ala Leu Val Arg Ala Thr Leu Leu Gly Trp Gly His
20     25     30
Arg Asn Leu Ser His Val Ala Gly Val Leu Asn Ala Ser Phe Leu Ala
35     40     45
His Phe Ile Lys Asp Pro Val Lys Thr Ala Lys Leu Ser His Lys Phe
50     55     60
Asn Asp Glu Arg Pro Tyr Pro Met Pro Ala Phe Ser Gln Phe Ser Asp
65     70     75     80
Gln Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys
85     90     95
Asn Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His
100    105    110
Ser Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu
115    120    125
Ala Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg
130    135    140
Ala Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys
145    150    155    160
Leu Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala
165    170    175
Gln Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys
180    185    190
His Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val
195    200    205
Leu Ser Phe Leu Ala Tyr Asp Trp Lys Arg Lys Val Trp Ser Glu Val
210    215    220
His
225

```

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...381

SUBSTITUTE SHEET (RULE 26)

1021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454

Thr	Trp	Arg	Tyr	Gln	Leu	Gly	Ser	Leu	Lys	Gly	Lys	Ile	Gln	Met	Ile
1				5					10					15	
Lys	Ser	Val	Glu	Ile	Glu	Asn	Tyr	Lys	Asn	Phe	Glu	His	Leu	Lys	Met
		20				25							30		
Glu	Asn	Phe	Lys	Leu	Ile	Asn	Phe	Phe	Thr	Gly	Gln	Asn	Asp	Ala	Gly
		35				40						45			
Lys	Thr	Asn	Leu	Leu	Glu	Ala	Leu	Tyr	Thr	Asn	Thr	Gly	Leu	Cys	Asp
	50				55						60				
Pro	Thr	Ala	Asn	Gln	Val	Ser	Leu	Pro	Pro	Glu	His	Ala	Val	Asn	Ile
	65			70						75				80	
Ser	Glu	Phe	Arg	Lys	Ile	Lys	Leu	Asp	Ala	Asp	Asn	Leu	Lys	Thr	Phe
			85					90					95		
Phe	Tyr	Gln	Gly	Asn	Thr	Ala	Asn	Pro	Ile	Ser	Ile	Arg	Thr	Glu	Phe
		100					105						110		
Glu	His	Ala	Thr	Ile	Pro	Leu	Thr	Ile	Gln	Tyr	Pro	Thr	Gln	Thr	Ser
	115					120					125				
Tyr	Ser	Lys	Asp	Ile	Asn	Leu	Asn	Ser	Asp	Asp	Ala	His	Met	Thr	Asn
	130				135						140				
Leu	Ile	Asn	Thr	Thr	Ile	Thr	Lys	Pro	Gln	Leu	Gln	Phe	Ser	Tyr	Asn
	145				150					155				160	
Pro	Ser	Leu	Ser	Pro	Met	Thr	Met	Thr	Tyr	Glu	Phe	Glu	Arg	Gln	Asn
			165					170					175		
Leu	Gly	Leu	Ile	His	Ser	Asn	Leu	Asp	Lys	Ile	Ala	Gln	Thr	Tyr	Lys
		180				185						190			
Glu	Asn	Ala	Met	Phe	Ile	Pro	Ile	Glu	Leu	Ser	Ile	Val	Asn	Ser	Leu
	195					200					205				
Lys	Ala	Leu	Glu	Asn	Leu	Gln	Leu	Ala	Ser	Lys	Glu	Lys	Glu	Leu	Ile
	210				215						220				
Glu	Ile	Leu	Gln	Cys	Phe	Asn	Pro	Asn	Ile	Leu	Asn	Ala	Asn	Thr	Ile
	225			230						235				240	
Arg	Lys	Ser	Val	Tyr	Ile	Gln	Ile	Lys	Asp	Glu	Asn	Thr	Pro	Leu	Glu
			245					250					255		
Glu	Ser	Pro	Lys	Arg	Leu	Leu	Asn	Leu	Phe	Gly	Trp	Gly	Phe	Ile	Lys
		260				265						270			
Phe	Phe	Ile	Met	Val	Ser	Ile	Leu	Ile	Asp	Asn	Arg	Val	Lys	Tyr	Leu
	275					280					285				
Phe	Ile	Asp	Glu	Ile	Glu	Ser	Gly	Leu	His	His	Thr	Lys	Met	Gln	Glu
	290				295						300				
Phe	Leu	Lys	Ala	Leu	Phe	Lys	Leu	Ala	Gln	Lys	Leu	Gln	Ile	Gln	Ile
	305			310						315				320	
Phe	Ala	Thr	Thr	His	Asn	Lys	Glu	Phe	Leu	Asn	Ala	Ile	Asn	Thr	
			325					330				335			
Ile	Ser	Asp	Asn	Glu	Thr	Gly	Val	Phe	Lys	Asp	Ile	Ala	Leu	Phe	Glu
		340				345						350			
Leu	Glu	Lys	Glu	Ser	Ala	Ser	Gly	Phe	Ile	Arg	His	Ser	Tyr	Ser	Met
	355					360					365				
Leu	Glu	Lys	Ala	Leu	Tyr	Arg	Gly	Met	Glu	Val	Arg	Gly			
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

1022

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455

```

Thr His Cys Leu Phe Leu Gly Gly Ser Ile Lys Ile Leu Leu Ile Leu
1      5      10      15
Lys Glu Gly Ile Asp Leu Asn His Gly Tyr Tyr Gln Leu Gly Lys Tyr
20      25      30
Thr Ile Lys Asp Asp Phe Ile Pro Ser Lys Lys Ala Val Val Glu Asp
35      40      45
Val Leu Ile Gln Ser Ser Asn Val Gly Met Ile Lys Ile Ser Lys Ser
50      55      60
Leu Asn Pro Glu Asp Phe Tyr Asn Gly Leu Leu Gly Tyr Gly Phe Ser
65      70      75      80
Gln Lys Thr Gly Ile Asp Leu Ser Leu Glu Ala Thr Gly Lys Ile Pro
85      90      95
Pro Leu Ser Ala Phe Lys Arg Glu Val Leu Lys Gly Ser Val Ser Tyr
100     105     110
Gly Tyr Gly Leu Asn Ala Thr Phe Leu Gln Leu Leu Arg Ala Tyr Ala
115     120     125
Val Phe Ser Asn Glu Gly Lys Leu Thr Thr Pro Tyr Leu Val Gln Arg
130     135     140
Glu Thr Ala Pro Asn Gly Asp Ile Tyr Ile Pro Ser Pro Lys Pro Thr
145     150     155     160
Phe Gln Val Ile Ser Pro Lys Ser Ala Arg Lys Met Lys Glu Thr Leu
165     170     175
Ile Lys Val Val Arg Tyr Gly Thr Gly Lys Asn Ala Gln Phe Glu Gly
180     185     190
Leu Tyr Ile Gly Gly Lys Thr Gly Thr Ala Arg Val Ala Lys Asn Gly
195     200     205
Ser Tyr Ser Ala Glu Ser Tyr Asn Ser Ser Phe Phe Gly Phe Ala Glu
210     215     220
Asp Glu Arg Gln Val Phe Thr Ile Gly Val Val Ile Leu Gly Ser His
225     230     235     240
Gly Lys Glu Glu Tyr Tyr Ala Ser Lys Ile Ala Ala Pro Ile Phe Lys
245     250     255
Glu Ile Thr Glu Ile Leu Val Arg Tyr Asn Tyr Leu Ser Pro Ser Ile
260     265     270
Ala Ile Gln Asn Ala Leu Glu Lys Asn Arg Leu Lys
275     280

```

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456

SUBSTITUTE SHEET (RULE 26)

1023

```

Asp Lys Lys Ile Leu Leu Ile Ile Gln Gly Lys Phe Met Glu Phe His
1      5      10      15
Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser Ala Leu Val Ala
20      25      30
Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile Val Phe Lys Leu
35      40      45
Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu Ser Ile Leu Ile
50      55      60
Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val Ser Ala Ser Phe
65      70      75      80
Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala Trp Ile Val Ile
85      90      95
Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser Gly Tyr Phe Glu
100      105      110
Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu Asp His Arg Ile Leu
115      120      125
Val Ile Leu Ile Gly Phe Cys Leu Ala His Phe
130      135

```

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457

```

Pro Lys Pro Lys Gly Val Cys Pro Lys Asn Leu Met Ser Lys Arg Ala
1      5      10      15
Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro Lys Pro Lys Ile Lys
20      25      30
Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala Tyr Pro Leu Lys Pro
35      40      45
His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser Leu Leu Ala Pro Ile
50      55      60
Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn Ala Ile Lys Pro Asp
65      70      75      80
Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met Pro Met Lys Ile Gln
85      90      95
Lys

```

(2) INFORMATION FOR SEQ ID NO:1458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1024

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458

```

Arg Asn Asp Phe Lys Gly Val Arg Lys Met Ala Leu Arg Val Leu Leu
1      5      10      15
Phe Phe Cys Phe Leu Phe Leu Gln Ala Glu Asp Lys Ser Gln Glu Leu
20      25      30
Ser Ser Ile Gln Lys Gln Met Ala Leu Val Asp Lys Lys Leu Ala Lys
35      40      45
Asp Asp Asn Val Trp Leu Lys Lys Phe Glu Asn Tyr Lys Ile Tyr Asn
50      55      60
Gln Ile Tyr Thr Glu Lys Glu Ser Val Arg Gln Glu Leu Arg Arg Leu
65      70      75      80
Lys Asn Lys Lys Ser Lys Asp Leu Leu Lys Ile Ser Thr Leu Glu His
85      90      95
Thr Leu Lys Ala Leu Glu Ser Gln Gln Lys Met Phe Glu Ser Tyr Gly
100     105     110
Val Asn Pro Phe Lys Asp Leu Ile Glu Arg Pro Asn Ile Pro Asn Ile
115     120     125
Pro Asn Ile Ala Asn Pro Ile Ala Ile Ile Asp Gly Ile Ser Phe Ile
130     135     140
Lys Ser Met Arg Leu Lys His Glu Asn Leu Lys Asn Asn Gln Thr Ser
145     150     155     160
Leu Gly Glu Val Leu Lys Leu Leu Asp Gln Lys His Gln Leu Leu Asn
165     170     175     180
Gln Trp His Ala Leu Asp Lys Ser Ala Lys Leu Ser Asp Glu Ile Tyr
180     185     190
Gln Thr Gln Ala Lys Arg Leu Glu Leu Gln Gly Ala Gln Asn Ile Leu
195     200     205
Lys Thr Thr Ile Gly Ile Phe Gln Lys Asp Ser Asp Glu Ala Ile Ser
210     215     220
Ile Val Lys Ser Gln Val Lys Asn Gln Leu Phe Lys Leu Val Tyr Val
225     230     235     240
Phe Leu Ala Ala Leu Leu Ser Val Val Phe Ala Trp Ile Leu Lys Ile
245     250     255
Ile Ser Ser Lys Tyr Ile Glu Asn Asn Glu Arg Val Tyr Thr Val Asn
260     265     270
Lys Ala Ile Asn Phe Val Asn Val Ser Val Ile Val Leu Ile Phe Leu
275     280     285
Phe Ser Tyr Leu Glu Asn Val Thr Tyr Leu Val Thr Val Leu Gly Phe
290     295     300
Ala Ser Ala Gly Leu Ala Ile Ala Met Lys Asp Leu Phe Met Ser Leu
305     310     315     320
Leu Gly Trp Phe Ile Ile Leu Ile Gly Gly Ser Val His Val Gly Asp
325     330     335
Arg Val Arg Ile Ala Lys Gly Thr Asp Ile Phe Ile Gly Asp Val Leu
340     345     350
Asp Ile Ser Met Leu His Ile Thr Ile Leu Glu Asp Val Thr Phe Thr
355     360     365
Thr Tyr Thr Asn Asn Arg Arg Ala Gly Arg Ile Ile Phe Val Pro Asn
370     375     380
Asn Tyr Ile Phe Thr Thr Met Phe Ala Asn Tyr Ser His Phe Gly Met
385     390     395     400
Lys Thr Val Trp Asp Gly Val Asp Phe Cys Val Thr Phe Asp Ser Asp
405     410     415
Phe Lys Lys Ala Ser Lys Ile Ala Leu Asn Ile Ala Thr Glu Leu Ser
420     425     430

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